

09. 803201

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2004, 15:29:33 ; Search time 39 Seconds
(without alignments)

471.215 Million cell updates/sec

Title: SEQ1
Perfect score: 976
Sequence: 1 CQEDSDIAFLIDGSGSIIP.....VNNFEALTIQNLREKXPA 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	976	100.0	1153	1 RWHUIB	cell surface glyco
2	756	77.5	1153	1 RWHUIB	leukocyte surface
3	550	56.4	1163	1 RWHUIB	cell surface glyco
4	328	33.6	1179	2 A53213	integrin alpha-E c
5	290.5	29.8	1170	2 S03308	cell surface glyco
6	268	27.5	1163	2 I56126	lymphocyte fuction
7	242	24.8	493	2 A33809	cartilage matrix p
8	235	24.1	500	2 S66522	cartilage matrix p
9	232	23.8	496	2 A37979	cartilage matrix p
10	217.5	22.3	1151	2 A45226	integrin alpha-1 c
11	215	22.0	3124	2 A40020	collagen alpha 1(X
12	214.5	22.0	1747	2 A45974	collagen alpha 1(X
13	214.5	22.0	1858	2 S31212	collagen alpha 1(X
14	214.5	22.0	1887	2 S78476	collagen alpha 1(X
15	207.5	21.3	272	2 A55348	integrin alpha-1 -
16	207.5	21.3	3051	2 S42373	hypothetical prote
17	202.5	20.7	1180	2 A35854	integrin alpha-1 c
18	191.5	19.6	741	2 T46488	hypothetical prote
19	188	19.3	929	2 I51027	type XII collagen
20	174.5	17.9	2944	2 A54849	collagen alpha 1(V
21	164	16.8	3176	2 CGHU3A	collagen alpha 3(V
22	162	16.6	3137	2 A37757	collagen alpha 3(V
23	161	16.5	1181	2 A33998	integrin alpha-2 c
24	160	16.4	1170	2 I45914	integrin alpha 2 s
25	156	16.0	1178	2 S44142	VLA-2 protein homo
26	146	15.0	550	2 T23760	hypothetical prote
27	143	14.7	843	2 A40970	undulin 1 - human
28	140.5	14.4	371	2 S32604	collagen alpha 2(V
29	137	14.0	763	2 I50807	complement factor

RESULT 1

RWHUIB

cell surface glycoprotein CD11b precursor [validated] - human
N:Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text change 09-Jul-2004
C:Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R:Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b)

A:Reference number: A31108; MUID:88315033; PMID:2457584

A:Accession: A31108

A:Molecule type: mRNA

A:Residues: 1-1153 <COR>

A:Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148

A:Note: part of this sequence was confirmed by protein sequencing

R:Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.

J. Cell Biol. 106, 2153-2158, 1988

A:Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor Mac-1

A:Reference number: A28915; MUID:88257215; PMID:2454931

A:Accession: A28915

A:Molecule type: mRNA

A:Residues: 1-499,501-965, 'P', 967-1153 <ARN>

A:Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA5945

A:Note: the authors translated the codon TAC for residue 1129 as Thr

A:Note: part of this sequence, including the amino end of the mature protein, was confirm

R:Shelley, C.S.; Arnaout, M.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991

A:Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regu

A:Reference number: A41600; MUID:92073318; PMID:1683702

A:Accession: A41600

A:Molecule type: DNA

A:Residues: 1-9 <SHE>

A:Cross-references: GB:IM76724; NID:g180018; PIDN:AAA58410.1; PID:g553215

R:Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988

A:Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi

A:Reference number: A94193; MUID:88190151; PMID:2833753

A:Accession: A30892

A:Molecule type: mRNA

A:Residues: 917-1042 <AR2>

A:Cross-references: GB:M18044

R:Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989

A:Title: cDNA sequence for the alphaM subunit of the human neutrophil adherence receptor

A:Reference number: A32218; MUID:89098893; PMID:2563162

A:Accession: A32218

A:Molecule type: mRNA

A:Residues: 9-1153 <HIC>

A:Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

A>Note: part of this sequence was confirmed by protein sequencing
 R: Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
 J. Immunol. 150, 480-490, 1993
 A:Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in
 n during evolution.
 A:Reference number: A46526; MUID:93123748; PMID:8419480
 A:Accession: A46526
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-499, 501-1153 <FLE>
 A:Cross-references: GB:552227; NID:G263047; PIDN:AA24821.1; PID:G263049
 A>Note: the last three bases of intron 13, CAG, are included in some but not all mature
 A>Note: sequence extracted from NCBI backbone (NCBI:121963)
 R:Pierce, M.W.; Renold-O'Donnell, E.; Todd III, R.F.; Arnaut, M.A.
 Biochim. Biophys. Acta 874, 368-371, 1986
 A:Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across sp
 A:Reference number: A90664; MUID:87076671; PMID:3539202
 A:Accession: A26091
 A:Molecule type: protein
 A:Residues: 17-31 <PIE>
 A:Experimental source: granulocytes
 R:Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
 Blood 79, 865-870, 1992
 A:Title: Characterization of the myeloid-specific CD11b promoter.
 A:Reference number: I52567; MUID:92144986; PMID:1346576
 A:Accession: I52567
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GB:M84477; NID:G180184; PIDN:AA51960.1; PID:G553219
 A:Comment: A common beta chain (CD-18) forms a heterodimer with this chain to form Mac-1
 C:Genetics:
 A:Gene: GDB:ITGAM; CR3A
 A:Cross-references: GDB:120599; OMIM:120980
 A:Map position: 16p11.2-16p11.2
 A>Note: promoter contains a GATA motif and two Spl consensus binding sites
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
 C:Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
 F:17-1108/Domain: extracellular #status predicted <EXT>
 F:148-318/Domain: von Willebrand factor type A repeat homology <VWA>
 F:468-478/Region: calcium/magnesium binding #status predicted
 F:530-538/Region: calcium/magnesium binding #status predicted
 F:593-601/Region: calcium/magnesium binding #status predicted
 F:1109-1134/Domain: transmembrane #status predicted <TM>
 F:1135-1153/Domain: intracellular #status predicted <INT>
 F:86,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding

Query Match 100.0%; Score 976; DB 1; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 5.1e-75;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 Db 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 180
 Db 264 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 323

Query Match 100.0%; Score 976; DB 1; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 5.1e-75;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 Db 204 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 180
 Db 264 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 323

RESULT 2
 S00551

leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse

N:Alternate names: complement-3 receptor alpha chain
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: S00551; I59078
 R:Pytel, R.
 EMBO J. 7, 1371-1378, 1988
 A:Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the ir
 A:Reference number: S00551; MUID:89312584; PMID:3044779
 A:Accession: S00551
 A:Molecule type: DNA
 A:Residues: 1-1153 <PYT>
 A:Cross-references: UNIPROT:P05555; EMBL:X07640; NID:G52982; PIDN:CAA30479.1; PID:G52983
 A>Note: the authors translated the codon CAC for residue 569 as Gln
 R:Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
 Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
 A:Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
 A:Reference number: I59078; MUID:86287312; PMID:2942940
 A:Accession: I59078
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 11-44 <RES>
 A:Cross-references: GB:M14293; NID:G198993; PIDN:AAA39484.1; PID:G554193
 C:Genetics:
 A:Gene: Mac-1
 C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
 C:Keywords: cell adhesion; glycoprotein; transmembrane protein
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental
 F:148-318/Domain: von Willebrand factor type A repeat homology <VWA>
 F:1106-1129/Domain: transmembrane #status predicted <TM>

Query Match 77.5%; Score 756; DB 2; Length 1153;
 Best Local Similarity 78.0%; Pred. No. 2.9e-56;
 Matches 149; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 Db 204 DPKRNPSPRSHVSPKQLNGRTKAGRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 180
 Db 264 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 323

Query Match 100.0%; Score 976; DB 1; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 5.1e-75;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDFRMKGFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPTQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 Db 204 DPKRNPSPRSHVSPKQLNGRTKAGRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 180
 Db 264 DPLGVEDVIPEADRGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVQVNNFEALKT 323

RESULT 3

RWU1C

cell surface glycoprotein CD11c precursor - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A36584; A35543; S00864

R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.

J. Biol. Chem. 265, 12750-12751, 1990

A:Reference number: A36584

A:Contents: erratum

A:Accession: A36584

A:Molecule type: DNA

A:Residues: 1-1163 <COR>

A:Cross-references: UNIPROT:P20702

A>Note: this revision to the sequence from reference A35543 includes the carboxyl end
 R:Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.

J. Biol. Chem. 265, 2782-2786, 1990

A:Title: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.

A:Reference number: A35543; MUID:90153906; PMID:2303426

A:Accession: A35543

A:Molecule type: DNA
A:Residues: 1-834 <C02>
A:Note: this sequence has been revised in reference A36584
R:Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Springer, T.A.
EMBO J. 6, 4023-4028, 1987
A:Title: CDNA cloning and complete primary structure of the alpha subunit of a leukocyte
A:Reference number: S00864; MUID:88166645; PMID:3327687
A:Accession: S00864
A:Molecule type: mRNA
A:Residues: 1-755, L, 757-1163 <C03>
A:Cross-references: GB:M81695; EMBL:Y00093; NID:G487829; PIDN:AAA59180.1; PID:G487830
A:Note: part of this sequence was confirmed by protein sequencing
C:Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on my
C:Genetics:
A:Gene: GDB:ITGAX; CD11C
A:Cross-references: GDB:119758; OMIM:151510
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
C:Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat;
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F:210-1107/Domain: extracellular #status predicted <EXT>
F:149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F:1108-1133/Domain: transmembrane #status predicted <TM>
F:1134-1163/Domain: intracellular #status predicted <INT>
F:61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 56.4%; Score 550; DB 1; Length 1163;
Best Local Similarity 56.0%; Pred. No. 1e-38;
Matches 107; Conservative 35; Mismatches 49; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQL--KISKTLFSLMQYSEEFRIHFTFK 60
DB 145 CPQEQDVLIDGSGSISRNZATVMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFE 204
QY 61 EFQNNPRSLVPIITQLGRTHTATGIRKVVRELFNTINGAKNAFKILVITDGEKFG 120
DB 205 EFRRTSNPLSLLASVHQLGFTTATAIQNVHRLPHASYGARRDATKILVITDGEK 264
QY 121 DPLGYDVIPEADREGVIRVYVGDAFRSEKSEKQELNTIASPPRDHVQVNNFEALKT 180
DB 265 DSLDYKDVIPADAAAGIIRVAGVGLAFQNFNSKWLNDIASKPSQEHIFKVEDFDALXD 324
QY 181 IQNQLREKXFA 191
DB 325 IQNQLKEKIFA 335
RESULT 4
A53213
Integrin alpha-E chain - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C:Accession: A53213
R:Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A:Title: Molecular cloning of the human mucosal lymphocyte integrin alpha (E) subunit. Un
A:Reference number: A53213; MUID:94164962; PMID:81119947
A:Accession: A53213
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1179 <SHA>
A:Cross-references: UNIPROT:P39570; GB:L25851; NID:G457244; PID:G457245
C:Genetics:
A:Gene: GDB:ITGAE
A:Map position: 17p13
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat-hom
F:199-371/Domain: von Willebrand factor type A repeat homology <VWA3>
Query Match 33.6%; Score 328; DB 2; Length 1179;
Best Local Similarity 38.8%; Pred. No. 8.7e-20;
Matches 71; Conservative 42; Mismatches 68; Indels 2; Gaps 1;

QY 6 SDIAFLIDGSGSIIPHDFRRMKFVSTVMEQL--KISKTLFSLMQYSEEFRIHFTFK 63
DB 201 TEAIIIDGSGSIDPPDFQRAKDFISNMNRFYKCFECFALVQYGGVITQTEFDLDSQ 260
QY 64 NNPNRSLVKIPIITQLGRTHTATGIRKVVRELFNTINGAKNAFKILVITDGEKFGDPL 123
DB 261 DVMAASLARVQNTIQVGSVTKTASAMQHVLDSIFTSSHSRRKASKVMVVLTDGGIFEDPL 320
QY 124 GYEDVPEADREGVIRVYVGDAFRSEKSEKQELNTIASPPRDHVQVNNFEALKTION 183
DB 321 NLTTVINSPKMQGVERFAIGVGBFKGARTARELNLIASDDETHAFKVTINMALDGLLS 380
QY 184 QLR 186
DB 381 KLR 383
RESULT 5
S03308
Cell surface glycoprotein CD11a precursor - human
N:Alternate names: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S03308; A47458; A47565; A48759; S36044
R:Larson, R.S.; Corbi, A.L.; Berman, L.; Springer, T.
J. Cell Biol. 108, 703-712, 1989
A:Title: Primary structure of the leukocyte function-associated molecule-1 alpha subunit:
A:Reference number: S03308; MUID:89139587; PMID:2537322
A:Accession: S03308
A:Molecule type: mRNA
A:Residues: 1-1170 <LAR>
A:Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:X00796; NID:G31421; PIDN:CAA6874
A:Note: part of this sequence was confirmed by protein sequencing
R:Corwell, R.D.; Gollahan, K.A.; Hickstein, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A:Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or CD11a) pr
A:Reference number: A47458; MUID:93248261; PMID:8097887
A:Accession: A47458
A:Molecule type: DNA
A:Residues: 1-20 <COR>
R:Shelley, C.S.; Farokhzad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5364-5368, 1993
A:Title: Identification of cell-specific and developmentally regulated nuclear factors th
A:Reference number: A47565; MUID:93281759; PMID:8099450
A:Accession: A47565
A:Molecule type: DNA
A:Residues: 1-20 <SHE>
A:Cross-references: GB:M95609
R:Nueda, A.; Lopez-Cabrera, M.; Vara, A.; Corbi, A.L.
J. Biol. Chem. 269, 19305-19311, 1993
A:Title: Characterization of the CD11a (alphaL, LFA-1alpha) integrin gene promoter.
A:Reference number: A48759; MUID:93374910; PMID:8103515
A:Accession: A48759
A:Molecule type: DNA
A:Residues: 1-20 <NUE>
A:Cross-references: EMBL:Z22804; NID:G311405; PIDN:CAA80461.1; PID:G311406
C:Genetics:
A:Gene: GDB:ITGAL; CD11A
A:Cross-references: GDB:119757; OMIM:153370
A:Map position: 16p11.2-16p11.2
C:Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C:Keywords: cell adhesion; cytoskeleton; glycoprotein; heterodimer; surface antigen; tra
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted <
F:154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 29.8%; Score 290.5; DB 2; Length 1170;
Best Local Similarity 32.6%; Pred. No. 1.4e-16;
Matches 62; Conservative 51; Mismatches 70; Indels 7; Gaps 2;
QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFK 60

Qy 180 TIQNLREKX 189
 Db 446 QIGKKLOKQI 455

RESULT 9
 A37979
 cartilage matrix protein precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
 C:Accession: A37979; B37979
 R:Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh
 J. Biol. Chem. 265, 19624-19631, 1990
 A>Title: Structure and chromosomal location of the human gene encoding cartilage matrix
 A:Reference number: A37979; PMID:91050568; PMID:2246248
 A:Accession: A37979
 A:Molecule type: DNA
 A:Residues: 1-496 <JEN>
 A:Cross-references: UNIPROT:P21941; GB:J05667
 A:Accession: B37979
 A:Molecule type: mRNA
 A:Residues: 157-290, 'L', 292-496 <JE2>
 A:Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1; PID:9
 C:Genetics:
 A:Gene: GDB:CE7M
 A:Cross-references: GDB:127280; OMIM:115437
 A:Map position: lp35-1p35
 A:Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
 C:Complex: homotrimer
 C:Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
 C:Keywords: glycoprotein; homotrimer
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-496/Product: cartilage matrix protein #status predicted <MAT>
 F:39-206/Domain: von Willebrand factor type A repeat homology <WVA1>
 F:273-437/Domain: EGF homology <EGF>
 F:227-262/Domain: von Willebrand factor type A repeat homology <WVA2>
 F:76,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:21-238,234-247,249-262/Disulfide bonds: #status predicted

Query Match 23.8%; Score 232; DB 2; Length 496;
 Best Local Similarity 29.5%; Pred. No. 4.5e-12;
 Matches 56; Conservative 43; Mismatches 73; Indels 18; Gaps 4;

Qy 6 SDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTL--FSLMQYSEERFIHFTKEFQ 63
 Db 274 TDLVFLIDGSKSVRPENFELVKKFIISIVDTLDSVSKLAQGLVQYSSVRQEPFLGRFH 333
 Qy 64 NNPNSRLVKPTIOLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
 Db 334 TKDKIAAVRNMSYMERGTMTGAALKYLIIDNSFTVSSGARGPGACKGVFTDGRS----- 388
 Qy 124 GYEDVIPADRE---GVIRVIGVDAFRSEKSRQELNTIASPPRDHVFQVNNPEALK 179
 Db 389 --QYINDAKKADLGFKMPAVGVGNV-----EDELREIASEPVAEHVYFADFTKTN 441

Qy 180 TIQNLREKX 189
 Db 442 QIGKKLOKQI 451

RESULT 10
 A45226
 integrin alpha-1 chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A45226
 R:Briesewitz, R.; Epstein, M.R.; Marcantonio, E.E.
 J. Biol. Chem. 268, 2989-2996, 1993
 A>Title: Expression of native and truncated forms of the human integrin alpha 1 subunit.
 A:Reference number: A45226; PMID:93155124; PMID:8428973
 A:Accession: A45226
 A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-1151 <BRI>
 A:Cross-references: UNIPROT:P56199
 A:Experimental source: hepatoblastoma cell line HepG2
 A>Note: sequence extracted from NCBI backbone (NCBI:P:124326)
 F:142-317/Domain: von Willebrand factor type A repeat homology <WVA1>

Query Match 22.3%; Score 217.5; DB 2; Length 1151;
 Best Local Similarity 30.6%; Pred. No. 2.2e-10;
 Matches 59; Conservative 39; Mismatches 84; Indels 11; Gaps 5;

Qy 7 DIAFLIDGSGSIIPHDFRMKEFVSTVMEQLK--KSKTLFSLMQYSEERFIHFTKEFQ 64
 Db 144 DIVIVLDGSGSIYPWD--SVTAFLNLLKRMIDIGFKQTQGVIGYGENVTHEFNLYSS 201
 Qy 65 NNPNSRLVKPTIOLLGR--THATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
 Db 202 TEEVLVAACKIVQRRGTMTALGDTTARKEAFTEARGARGVKVWVIVTDGESH-DNH 260
 Qy 124 GYEDVIPADREGVIRVIGVDAFR-----SEKSRQELNTIASPPRDHVFQVNNPEAL 178
 Db 261 RLKVKVIQCEDENIQRFSAILGSGVNRGNLSTEFVEIKSIASEPTEKHFENVSDLEAL 320
 Qy 179 KTIONQLREKXFA 191
 Db 321 VTIVKTLGERIFA 333

RESULT 11
 A40020
 collagen alpha 1(XII) chain precursor - chicken
 N:Alternate names: fibrochimerin
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A40020; A34485; A28037; S23814; S22254; S28811
 R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obari
 J. Cell Biol. 115, 209-221, 1991
 A>Title: The complete primary structure of type XII collagen shows a chimeric molecule w
 nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp sice.
 A:Reference number: A40020; PMID:92011862; PMID:1918137
 A:Accession: A40020

A:Molecule type: mRNA
 A:Residues: 1-3124 <YAN>
 A:Cross-references: UNIPROT:P13944; GB:D00824; NID:9222810; PIDN:BA00701.1; PID:G2222811
 A>Note: In the authors' translation residues 1216-1219 are shown after residue 1235 and,
 R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
 J. Biol. Chem. 264, 19772-19778, 1989
 A>Title: Type XII collagen. A large multidomain molecule with partial homology to type I
 A:Reference number: A34485; PMID:90062079; PMID:2584192
 A:Accession: A34485
 A:Molecule type: mRNA
 A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
 A:Cross-references: EMBL:J05137; NID:G211284; PIDN:AAA48635.1; PID:G211285
 A:Accession: B34485
 A:Molecule type: protein
 A:Residues: 2772-2792/2846-2873 <GOR2>
 R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
 A>Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c
 A:Reference number: A28037; PMID:87317590; PMID:3476925
 A:Accession: A28037
 A:Molecule type: mRNA
 A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
 A:Cross-references: EMBL:M17375; NID:G211649; PIDN:AAA48718.1; PID:G211650
 A>Note: this sequence has been revised in reference A34485
 R:Koch, M.; Bernasconi, C.; Chiquet, M.
 Eur. J. Biochem. 207, 847-856, 1992
 A>Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of t
 A:Reference number: S23814; PMID:92362621; PMID:1323460
 A:Accession: S23814
 A:Molecule type: protein
 A:Residues: 'X', 1333, 'Q', 1335-1347, 1914-1928, 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <C
 R:Dublet, B.; van der Rest, M.

J. Biol. Chem. 262, 17724-17727, 1987
A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-
A:Reference number: S22254; MUID:88087065; PMID:3121603
A:Accession: S22254
A:Molecule type: protein
A:Residues: 2831-2832, 'T', 2834, 'R', 2836-2843, 3002-3014 <DUB>
R:Trueb, J.; Trueb, B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A:Title: The two splice variants of collagen XII share a common 5' end.
A:Reference number: S28811; MUID:93042014; PMID:1420368
A:Accession: S28811
A:Molecule type: mRNA
A:Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
A:Cross-references: EMBL:X67327
C:Genetics:
A:Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C:Keywords: alternative splicing; cell binding; coiled coil; connective tissue; disulfid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F:24, 1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted
F:24-114/Domain: IIR #status predicted <IIR>
F:24-105/Domain: fibronectin type III repeat homology <FN3A>
F:137-301/Domain: von Willebrand factor type A repeat homology <VWA1>
F:332-425/Domain: IIR #status predicted <IIR>
F:332-414/Domain: fibronectin type III repeat homology <FN3B>
F:437-601/Domain: von Willebrand factor type A repeat homology <VWA2>
F:629-1178/Domain: IIR #status predicted <IIR>
F:630-711/Domain: fibronectin type III repeat homology <FN3C>
F:721-802/Domain: fibronectin type III repeat homology <FN3D>
F:812-895/Domain: fibronectin type III repeat homology <FN3E>
F:905-986/Domain: fibronectin type III repeat homology <FN3F>
F:995-1076/Domain: fibronectin type III repeat homology <FN3G>
F:1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F:1197-1361/Domain: von Willebrand factor type A repeat homology <VWA3>
F:1384-2295/Domain: IIR #status predicted <IIR>
F:1474-1557/Domain: fibronectin type III repeat homology <FN3I>
F:1566-1647/Domain: fibronectin type III repeat homology <FN3J>
F:1655-1738/Domain: fibronectin type III repeat homology <FN3K>
F:1756-1838/Domain: fibronectin type III repeat homology <FN3L>
F:1847-1828/Domain: fibronectin type III repeat homology <FN3M>
F:1937-2019/Domain: fibronectin type III repeat homology <FN3P>
F:2028-2110/Domain: fibronectin type III repeat homology <FN3Q>
F:2119-2199/Domain: fibronectin type III repeat homology <FN3R>
F:2207-2294/Domain: fibronectin type III repeat homology <FN3S>
F:2325-2490/Domain: von Willebrand factor type A repeat homology <VWA4>
F:2438-2440/Region: cell adhesion #status predicted
F:2509-2750/Domain: IIR, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domain: collagenous NC2 #status predicted <COL2>
F:2899-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domain: collagenous NC1 #status predicted <COL1>
F:3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>
F:32, 1006, 1032, 1044, 1512, 1767, 2210, 2273, 2532, 2603/Binding site: carbohydrate (Asn) (cova
F:2780, 2789, 2836, 2842, 2860, 2866, 2869, 3004, 3007/Modified site: hydroxyproline (Pro) #stat

Query Match 22.0%; Score 215; DB 2; Length 3124;
Best Local Similarity 30.6%; Pred. No. 1.3e-09;
Matches 57; Conservative 37; Mismatches 74; Indels 18; Gaps 4;
QY 6 SDIAPLIDSGSIIPHDFRMRKEFVSTWME--QLKSKTFLPSLMQYSEEFRIHFTFEQF 63
DB 138 TDLVFLVDGWSVGRNFRYLDLFWALVSAFDIGEKTRVGVVQVSSDRTFENLQYF 197
QY 64 NNPFRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPL 123
DB 198 RRSLLDAIKRIPYKGGNTWTGEALDVLKNTFTESAGARKFPKVAIVITDGA----- 252
QY 124 GYEDVIPADRE----GVIRVIGVDGAFREKSRQELNITASPPDRHVFQVNNFPAK 179
DB 253 --QDEVEIPARELNIGVEVSLGKAA-----DAKELKLIASQPSLKHVFNANFDGIV 305

QY 180 TIONQL 185
DB 306 DIQNEI 311
RESULT 12
A45974
collagen alpha 1(XIV) chain precursor, short form 2 - chicken
N:Alternate names: undulin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: A45974; S30085; S22916; S17035; S20833
R:Grecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lina
J. Biol. Chem. 268, 12177-12184, 1993
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' regions
ns.
A:Reference number: A45974; MUID:93280195; PMID:8505337
A:Accession: A45974
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-1747 <GER>
A:Cross-references: UNIPROT:P32018
A:Experimental source: embryo skin
A:Note: sequence inconsistent with the nucleotide translation
R:Apfe, S.S.
Submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30085
A:Molecule type: mRNA
A:Residues: 1472-1660 <APT>
A:Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G938175
R:Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A:Title: Type XIV collagen is a variant of undulin.
A:Reference number: S22916; MUID:92339443; PMID:1339349
A:Accession: S22916
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, F
Eur. J. Biochem. 201, 333-338, 1991
A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A:Reference number: S17035; MUID:92037585; PMID:1935930
A:Accession: S17035
A:Molecule type: mRNA
A:Residues: 1472-1659 <GOR1>
A:Accession: S20833
A:Molecule type: protein
A:Residues: 1551-1570; 1593-1599; 1639-1667 <GOR2>
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F:40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:236-317/Domain: fibronectin type III repeat homology <FN3A>
F:326-409/Domain: fibronectin type III repeat homology <FN3B>
F:418-498/Domain: fibronectin type III repeat homology <FN3C>
F:507-591/Domain: fibronectin type III repeat homology <FN3D>
F:625-707/Domain: fibronectin type III repeat homology <FN3E>
F:716-798/Domain: fibronectin type III repeat homology <FN3F>
F:806-893/Domain: fibronectin type III repeat homology <FN3G>
F:924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F:1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F:1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>
Query Match 22.0%; Score 214.5; DB 2; Length 1747;
Best Local Similarity 32.4%; Pred. No. 6.7e-10;
Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;
QY 1 CQEDSDTAFLIDGSGSIIPHDFRMRKEFV-STV--MEQLKSKTFLPSLMQYSEEFRIHP 57
DB 920 CKAARADLVFLVDGWSVGRNFRYLDLFWALVSAFDIGEKTRVGVVQVSSDRTFENLQYF 979
QY 58 TFEQFNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGE 117

Db 980 KLNAYTKETLLFAIQIAYKGGNTGTGKAIKHAREVLTGEGMRKGIPIKVLVWITDGR 1039
 QY 118 KFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNFEA 177
 Db 1040 SQDD---VNVKVSREMQLDGSFPAIGVADADYS-----ELVNIQSKPSERHVFVDDFDA 1091
 QY 178 LKTIQNQL 185
 Db 1092 FTKIEDEL 1099

RESULT 13

S31212
 collagen alpha 1(XIV) chain precursor, short form - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
 C/Accession: S31212
 R/Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
 Eur. J. Biochem. 212, 483-490, 1993
 A/Title: Complete primary structure of chicken collagen XIV.
 A/Reference number: S31211; MUID:93185668; PMID:8444186
 A/Accession: S31212
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-1857 <WAE>
 A/Cross-references: EMBL:X70792; NID:G288874; PIDN:CAA50063.1; PID:G288875
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 C/Genetics:
 A/Gene: Col14A1

C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
 F/1-28/Domain: signal sequence #status predicted <SIG>
 F/29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT>
 F/29-110/Domain: fibronectin type III repeat homology <FN3A>
 F/352-433/Domain: von Willebrand factor type A repeat homology <FN3B>
 F/442-525/Domain: fibronectin type III repeat homology <FN3C>
 F/534-614/Domain: fibronectin type III repeat homology <FN3D>
 F/623-707/Domain: fibronectin type III repeat homology <FN3E>
 F/741-823/Domain: fibronectin type III repeat homology <FN3F>
 F/832-914/Domain: fibronectin type III repeat homology <FN3G>
 F/922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F/1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1857;
 Best Local Similarity 32.4%; Pred. No. 7.2e-10;
 Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPQSDSDIAFLIDGSGSIIPHDFRMKEFV-STV--MEQLKSKTLPFLSMQYSEFRHIF 57
 Db 1036 CKAADLVFLVDGSGISGDDNFNKKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTF 1095
 QY 58 TFKEFQNNPNSLVKPIITQLGRTHGTATGIRKVVRELFNITGARKNAFKILVITDGE 117
 Db 1096 KLNAYTKETLLFAIQIAYKGGNTGTGKAIKHAREVLTGEGMRKGIPIKVLVWITDGR 1155
 QY 118 KFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNFEA 177
 Db 1156 SQDD---VNVKVSREMQLDGSFPAIGVADADYS-----ELVNIQSKPSERHVFVDDFDA 1207
 QY 178 LKTIQNQL 185
 Db 1208 FTKIEDEL 1215

RESULT 14

S78476
 collagen alpha 1(XIV) chain precursor, long form - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
 C/Accession: S78476; S31211
 R/Trueb, B.
 submitted to the EMBL Data Library, January 1993

A/Reference number: S78476
 A/Accession: S78476
 A/Molecule type: mRNA
 A/Residues: 1-1888 <TRU>
 A/Cross-references: UNIPROT:P32018; EMBL:X70793; NID:G288872; PIDN:CAA50064.1; PID:G28888;
 R/Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
 Eur. J. Biochem. 212, 483-490, 1993
 A/Title: Complete primary structure of chicken collagen XIV.
 A/Reference number: S31211; MUID:93185668; PMID:8444186
 A/Accession: S31211
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-416;1460-1811,1843-1888 <WAE>
 A/Cross-references: EMBL:X70793
 C/Genetics:
 A/Gene: Col14A1

C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
 F/1-28/Domain: signal sequence #status predicted <SIG>
 F/29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
 F/29-110/Domain: fibronectin type III repeat homology <FN3A>
 F/352-433/Domain: von Willebrand factor type A repeat homology <FN3B>
 F/442-525/Domain: fibronectin type III repeat homology <FN3C>
 F/534-614/Domain: fibronectin type III repeat homology <FN3D>
 F/623-707/Domain: fibronectin type III repeat homology <FN3E>
 F/741-823/Domain: fibronectin type III repeat homology <FN3F>
 F/832-914/Domain: fibronectin type III repeat homology <FN3G>
 F/922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F/1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 22.0%; Score 214.5; DB 2; Length 1888;
 Best Local Similarity 32.4%; Pred. No. 7.4e-10;
 Matches 61; Conservative 31; Mismatches 85; Indels 11; Gaps 4;

QY 1 CPQSDSDIAFLIDGSGSIIPHDFRMKEFV-STV--MEQLKSKTLPFLSMQYSEFRHIF 57
 Db 1036 CKAADLVFLVDGSGISGDDNFNKKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTF 1095
 QY 58 TFKEFQNNPNSLVKPIITQLGRTHGTATGIRKVVRELFNITGARKNAFKILVITDGE 117
 Db 1096 KLNAYTKETLLFAIQIAYKGGNTGTGKAIKHAREVLTGEGMRKGIPIKVLVWITDGR 1155
 QY 118 KFGDPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNFEA 177
 Db 1156 SQDD---VNVKVSREMQLDGSFPAIGVADADYS-----ELVNIQSKPSERHVFVDDFDA 1207
 QY 178 LKTIQNQL 185
 Db 1208 FTKIEDEL 1215

RESULT 15

A53348
 integrin alpha-1 - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C/Accession: A53348
 R/Kern, A.; Briesewitz, R.; Bank, I.; Marcantonio, E.E.
 J. Biol. Chem. 269, 22811-22816, 1994
 A/Title: The role of the I domain in ligand binding of the human integrin alpha-1beta-1.
 A/Reference number: A53348; MUID:94357330; PMID:7521332
 A/Accession: A53348
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-272 <KER>
 A/Cross-references: UNIPROT:O42094; GB:U10114
 F/55-230/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 21.3%; Score 207.5; DB 2; Length 272;
 Best Local Similarity 29.5%; Pred. No. 2.6e-10;
 Matches 57; Conservative 39; Mismatches 86; Indels 11; Gaps 5;

QY 7 DIAFLIDGSGSIIPHDFRMKEFVSTVMEQLK--KSKTLFSLMQYSEFRHIFTFKFEQN 64

```

Db      57 DIVIVLDGNSIYP--WESVTAFNSLLNMDIGPQQTQVGIVQYQGTWVHEFYINTYST 114
QY      65 NENPRSLVKPITQLLG-RTHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPL 123
Db      115 TEEVMDAALRIQRGGTQTM TALGIDTAREEAFTGAHGARRGVQKVMVIVTDGESH-DNY 173
QY      124 GYEDVIPEADREGVIRYVIGVDAP----RSEKSRQELNTIASKPPRDHVQVNNFEAL 178
Db      174 RLQEVIDKCEDENIORFAILGSYRGNLSTEFVEEIKSIASAKTEKHFNVSDIAL 233
QY      179 KTIQNLREKXFA 191
Db      234 VTIVEALGERIFA 246

```

Search completed: November 9, 2004, 15:37:29
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2004, 15:29:31 ; Search time 207 Seconds
(without alignments)
530.901 Million cell updates/sec

Title: SEQ1

Perfect score: 976

Sequence: 1 CQEDSDIAFLIDGSGSIIP.....VNNFEALTIQNQREKXFA 191

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	976	100.0	1152	1 ITAM HUMAN	P11215 homo sapien
2	788	80.7	920	2 Q28984	Q28984 sus scrofa
3	756	77.5	1153	1 ITAM MOUSE	P05555 mus musculus
4	729	74.7	1151	2 Q9J130	Q9J130 rattus norv
5	605	62.0	1161	1 ITAD RAT	Q9QY67 rattus norv
6	593	60.8	205	2 Q63001	Q63001 rattus norv
7	593	60.8	1162	1 ITAD HUMAN	Q13349 homo sapien
8	550	56.4	1163	1 ITAX HUMAN	P20702 homo sapien
9	544	55.7	1188	2 Q6KA54	Q6KA54 mus musculus
10	544	55.7	1188	2 BAD21383	Bad21383 mus muscu
11	543	55.6	1189	1 ITAX MOUSE	Q9QY84 mus musculus
12	408	41.8	304	2 Q6P666	Q6P666 mus musculus
13	408	41.8	304	2 AAH57200	AAH57200 mus muscu
14	344	35.2	895	2 Q9WJF8	Q9WJF8 mus sp. iig
15	344	35.2	1167	2 Q88340	Q88340 rattus norv
16	341	34.9	1038	2 Q8BS01	Q8BS01 mus musculus
17	338	34.6	1157	1 ITAE MOUSE	Q60577 mus musculus
18	328	33.6	1179	1 ITAE HUMAN	P38570 homo sapien
19	327	33.5	1160	2 Q8MKF4	Q8MKF4 felis silve
20	323.5	33.1	1167	2 Q88341	Q88341 rattus norv
21	319	32.7	231	2 Q8N882	Q8N882 homo sapien
22	304	31.1	79	2 Q8HY27	Q8HY27 ovis aries
23	304	31.1	79	2 Q8HY41	Q8HY41 bos taurus
24	294.5	30.2	1170	1 ITAL HUMAN	P20701 homo sapien
25	287.5	29.5	1165	1 ITAL BOVIN	P61625 bos taurus
26	282	28.9	269	2 Q8OWE9	Q8OWE9 rattus norv
27	268	27.5	1160	2 Q9R200	Q9R200 mus musculus
28	268	27.5	1161	2 Q9WTV4	Q9WTV4 mus musculus
29	268	27.5	1163	1 ITAL MOUSE	P24063 mus musculus
30	267.5	27.4	1196	2 Q98TF1	Q98TF1 cyprinus ca
31	263.5	27.0	1166	2 Q6TYB8	Q6TYB8 bos taurus

ALIGNMENTS

RESULT 1

ID	ITAM_HUMAN	STANDARD;	PRT;	1152 AA.
AC	P11215;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor M01)			
DE	(Neutrophil adherence receptor)			
GN	Name=ITGAM; Synonyms=CR3A, CD11B;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88315033; PubMed=2457584;			
RA	Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;			
RT	"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";			
RL	J. Biol. Chem. 263:12403-12411(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88190151; PubMed=2833753;			
RA	Arnaut M.A., Renold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.;			
RT	"Molecular cloning of the alpha subunit of human and guinea pig leukocyte adhesion glycoprotein M01: chromosomal localization and homology to the alpha subunits of integrins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88257215; PubMed=2454931;			
RA	Arnaut M.A., Gupta S.K., Pierce M.W., Tenen D.G.;			
RT	"Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M01 (complement receptor type 3).";			
RL	J. Cell Biol. 106:2153-2158(1988).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93123748; PubMed=8419480;			
RA	Fleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.;			
RT	"Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during evolution.";			
RL	J. Immunol. 150:480-490(1993).			
RN	[5]			
RP	SEQUENCE OF 9-1153 FROM N.A.			
RX	MEDLINE=89098993; PubMed=2563162;			
RA	Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L., Roth G.J.;			
RT	"cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";			

32	263.5	27.0	1166	2	AAQ90015	AaQ90015 bos tauru
33	253.5	26.0	1187	2	Q98TF0	Q98TF0 cyprinus ca
34	242	24.8	493	1	CAMA_CHICK	P05099 gallus gall
35	238	24.4	257	2	Q8C270	Q8C270 mus musculu
36	237	24.3	652	2	Q95L12	Q95L12 bos taurus
37	235	24.1	500	1	CAMA_MOUSE	P51942 mus musculu
38	235	24.1	500	2	Q8OVN5	Q8OVN5 mus musculu
39	232	23.8	496	1	CAMA_HUMAN	P21941 homo sapien
40	231	23.7	656	2	Q96DT1	Q96DT1 homo sapien
41	231	23.7	678	2	Q9UDN0	Q9UDN0 homo sapien
42	231	23.7	678	2	AAQ88704	AaQ88704 homo sapi
43	231	23.7	693	2	Q96DM8	Q96DM8 homo sapien
44	228.5	23.4	1086	2	Q96H31	Q96H31 homo sapien
45	224.5	23.0	589	2	Q7ZX63	Q7ZX63 xenopus lae

RL Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
RN [6] SEQUENCE OF 1-9 FROM N.A.
RP MEDLINE=92073318; PubMed=1683702;
RX Shelley C.S., Arnaut M.A.;
RA "The promoter of the CD11b gene directs myeloid-specific and
RT developmentally regulated expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
RN [7] SEQUENCE OF 1-9 FROM N.A.
RP TISSUE=Blood;
RX MEDLINE=92144986; PubMed=1346576;
RA Pahl H.L., Rosmarin A.G., Tenen D.G.;
RT "Characterization of the myeloid-specific CD11b promoter.";
RN [8] Blood 79:865-870(1992).
RP SEQUENCE OF 17-31.
RX MEDLINE=87076671; PubMed=3539202;
RA Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaut M.A.;
RT "N-terminal sequence of human leukocyte glycoprotein Mol: conservation
RN across species and homology to platelet IIb/IIIa.";
RL Biochim. Biophys. Acta 874:368-371(1986).
RP SEQUENCE OF 17-31.
RX MEDLINE=95171458; PubMed=7867070;
RA Lee J.O., Rieu P., Arnaut M.A., Liddington R.;
RT "Crystal structure of the A domain from the alpha subunit of integrin
RN CR3 (CD11b/CD18).";
RL Cell 80:631-638(1995).
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
RX MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RN activation?";
RL Structure 3:1333-1340(1995).
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
RX MEDLINE=96363671; PubMed=8747460;
RA Lee J.O., Bankston L.A., Arnaut M.A., Liddington R.C.;
RT "Two conformations of the integrin A-domain (I-domain): a pathway for
RN activation?";
RL Structure 3:1333-1340(1995).
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
RX MEDLINE=96362595; PubMed=9687375;
RA Baldwin E.T., Saver R.W., Bryant G.L. Jr., Curry K.A.,
RA Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
RA Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E.,
RA Muchler V.T., Tomich C.S., Wetenpaugh K.D., Wiley V.H.;
RT "Cation binding to the integrin CD11b I domain and activation model
RN assessment.";
RL Structure 6:923-935(1998).
RP 3D-STRUCTURE MODELING OF 17-616.
RX MEDLINE=98226734; PubMed=9560195;
RA Oxvig C., Springer T.A.;
RT "Experimental support for a beta-propeller domain in integrin alpha-
RN subunits and a calcium binding site on its lower surface.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).
CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
CC adhesive interactions of monocytes, macrophages and granulocytes
CC as well as in mediating the uptake of complement-coated particles.
CC It is identical with CR-3, the receptor for the iC3b fragment of
CC the third complement component. It probably recognizes the R-G-D
CC peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
CC fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
CC of fibrinogen gamma chain.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
CC associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
CC granulocytes.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWF domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWF domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".

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CC
EMBL; J03925; AAA59544.1; -;
DR EMBL; M18044; AAA59491.1; -;
DR EMBL; J04145; AAA59903.1; -;
DR EMBL; S52237; AAB24821.1; -;
DR EMBL; S52152; AAB24821.1; JOINED.
DR EMBL; S52153; AAB24821.1; JOINED.
DR EMBL; S52154; AAB24821.1; JOINED.
DR EMBL; S52155; AAB24821.1; JOINED.
DR EMBL; S52157; AAB24821.1; JOINED.
DR EMBL; S52159; AAB24821.1; JOINED.
DR EMBL; S52161; AAB24821.1; JOINED.
DR EMBL; S52164; AAB24821.1; JOINED.
DR EMBL; S52165; AAB24821.1; JOINED.
DR EMBL; S52167; AAB24821.1; JOINED.
DR EMBL; S52169; AAB24821.1; JOINED.
DR EMBL; S52170; AAB24821.1; JOINED.
DR EMBL; S52173; AAB24821.1; JOINED.
DR EMBL; S52174; AAB24821.1; JOINED.
DR EMBL; S52180; AAB24821.1; JOINED.
DR EMBL; S52181; AAB24821.1; JOINED.
DR EMBL; S52184; AAB24821.1; JOINED.
DR EMBL; S52189; AAB24821.1; JOINED.
DR EMBL; S52191; AAB24821.1; JOINED.
DR EMBL; S52192; AAB24821.1; JOINED.
DR EMBL; S52203; AAB24821.1; JOINED.
DR EMBL; S52212; AAB24821.1; JOINED.
DR EMBL; S52213; AAB24821.1; JOINED.
DR EMBL; S52216; AAB24821.1; JOINED.
DR EMBL; S52219; AAB24821.1; JOINED.
DR EMBL; S52220; AAB24821.1; JOINED.
DR EMBL; S52221; AAB24821.1; JOINED.
DR EMBL; S52222; AAB24821.1; JOINED.
DR EMBL; S52226; AAB24821.1; JOINED.
DR EMBL; M76724; AAA58410.1; -;
DR EMBL; M64477; AAA51960.1; -;
DR PIR; A31108; RWU1B.
DR PDB; 1A8X; Model; @=17-1152.
DR PDB; 1BHO; X-ray; 1/2=-.
DR PDB; 1BHQ; X-ray; 1/2=-.
DR PDB; 1IDN; X-ray; 1/2=-.
DR PDB; 1IDO; X-ray; @=140-331.
DR PDB; 1JLM; X-ray; @=143-334.
DR PDB; 1MIU; X-ray; A=137-331.
DR PDB; 1MF7; X-ray; A=144-337.
DR PDB; 1N92; X-ray; A=140-335.
DR PDB; 1NA5; X-ray; A=144-345.
DR Genew; HGNC:6149; ITGAM.
DR MIM; 120980; -.
DR GO; GO:0008305; C: integrin complex; TAS.
DR GO; GO:0007155; P: cell adhesion; TAS.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS00234; VWA; 1.
DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
KW Transmembrane.

```
FT SIGNAL 1 16 Integrin alpha-M.
FT CHAIN 17 1152

Query Match 100.0%; Score 976; DB 1; Length 1152;
Best Local Similarity 99.5%; Pred. No. 2.8e-70;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFEVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFRRMKFEVSTVMEQLKSKTLFSLMQYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPIPTQLGRHTATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPIPTQLGRHTATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRVYGVGDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALTK 180
DB 264 DPLGYEDVPEADREGVIRVYGVGDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALTK 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKXFA 334

RESULT 2
Q28984 PRELIMINARY; PRT; 920 AA.
AC Q28984;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CD1lb (Fragment).
GN Names=CD1lb;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee J.-K., Schock L.B., Rutherford M.S.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
DR EMBL; U40072; AAB16869.1; -
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; P:cell-matrix adhesion; IEA.
DR InterPro; IPR002035; VWF_4.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 4.
DR SMART; SM00327; VWA; 1.
DR SMART; SM00327; VWA; 1.
KW Cell adhesion; Integrin; Transmembrane.
FT NON_TER 1
FT NON_TER 920
FT NON_TER 920
SQ SEQUENCE 920 AA; 102440 MW; E96CC51E350DD5AC CRC64;

Query Match 80.7%; Score 788; DB 2; Length 920;
Best Local Similarity 80.6%; Pred. No. 3.7e-55;
Matches 154; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFEVSTVMEQLKSKTLFSLMQYSEFRHFTFK 60
DB 11 CPQEDSDIAFLIDGSGSIIPHDFRRMKFEVSTVMEQLKSKTLFSLMQYSEFRHFTFK 70
QY 61 EFQNNPNRSLVKPIPTQLGRHTATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
DB 71 DFRNESPFLVLRPIPTQLGRHTATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 130
QY 121 DPLGYEDVPEADREGVIRVYGVGDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALTK 180
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DB 131 DPLGYEDVPEADRKGVIRVYGVGDAPFNWKSREELNTIASPCGDHVFQVNNFEAVKT 190
QY 181 IQNQLREKXFA 191
DB 191 IQNQLREKXFA 201

RESULT 3
ITAM MOUSE STANDARD; PRT; 1153 AA.
AC P05555; Q8CA73;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).
GN Name=Itgam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88312584; PubMed=3044779;
RA Pytela R.;
RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von Willebrand factor."
RT Willebrand factor."
RL EMBO J. 7:1371-1378 (1988).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Spinal cord; DOI=10.1038/nature01266;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Buit C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shibata K., Kagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havaishizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
RT Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE OF 11-45 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=8628712; PubMed=2942940;
RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E.,
RA Larson R.S., Roberts T.M., Springer T.A.;
RT "A partial genomic DNA clone for the alpha subunit of the mouse complement receptor type 3 and cellular adhesion molecule Mac-1."
RT Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648 (1986).
RN [4]
```

SEQUENCE OF 17-28.
 RX MEDLINE=85188276; PubMed=3887182;
 RA Springer T.A., Teplow D.B., Dreyer W.J.,
 RT "Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
 glycoproteins and unexpected relation to leukocyte interferon.";
 RL Nature 314:540-542(1985).
 CC -!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
 adhesive interactions of monocytes, macrophages and granulocytes
 as well as in mediating the uptake of complement-coated particles.
 It is identical with CR-3, the receptor for the iC3b fragment of
 the third complement component. It probably recognizes the R-G-D
 peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
 fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
 of fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in
 mast cell development and in immune complex-mediated
 glomerulonephritis. Mice expressing a null mutation of the alpha-M
 subunit gene demonstrate increase in neutrophil accumulation, in
 response to a impaired degranulation and phagocytosis, events that
 apparently accelerate apoptosis in neutrophils. These mice develop
 obesity.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
 associates with beta-2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=P05555-1; Sequence=Displayed;
 Name=2;
 IsoId=P05555-2; Sequence=VSP_010473;
 Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
 granulocytes.
 CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
 with I-domains do not undergo protease cleavage.
 CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -!- SIMILARITY: Contains 1 VWFA domain.
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 or send an email to license@isb-sib.ch)

 DR EMBL; X07640; CAA30479.1; -.
 DR EMBL; AK039444; BAC30350.1; -.
 DR EMBL; M14293; AAA39484.1; -.
 DR PIR; S00551; S00551.
 DR HSSP; P11215; 1BHO.
 DR MGD; MGI:96607; Itgam.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.
 DR GO; GO:0007155; P:cell adhesion; IMP.
 DR GO; GO:0045123; P:cellular extravasation; IMP.
 DR GO; GO:0030593; P:neutrophil chemotaxis; IMP.
 DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF A.
 DR Pfam; PF01839; FG-GAP; 3_
 DR Pfam; PF00357; Integrin_alpha; 1.
 DR Pfam; PF00092; VWA; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00191; Int_alpha; 5.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS02334; VWFA; 1.
 KW Alternative splicing; Calcium; Cell adhesion;
 KW Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 1153
 FT DOMAIN 17 1105
 Integrin alpha-M.
 Extracellular (Potential).

FT	TRANSMEM	1106	1129	Potential.
FT DOMAIN	1130	1153		Cytoplasmic (Potential).
FT REPEAT	31	84		FG-GAP 1.
FT REPEAT	85	163		FG-GAP 2.
FT DOMAIN	164	350		VWFA.
FT REPEAT	337	400		FG-GAP 3.
FT REPEAT	401	452		FG-GAP 4.
FT REPEAT	454	515		FG-GAP 5.
FT REPEAT	517	575		FG-GAP 6.
FT REPEAT	580	632		FG-GAP 7.
FT CA_BIND	465	473		Potential.
FT CA_BIND	529	537		Potential.
FT CA_BIND	532	600		Potential.
FT SITE	1132	1136		GFFR motif.
FT DISULFID	66	73		By similarity.
FT DISULFID	105	123		By similarity.
FT DISULFID	654	711		By similarity.
FT DISULFID	770	776		By similarity.
FT DISULFID	959	1023		By similarity.
FT DISULFID	1028	1033		By similarity.
FT CARBOHYD	58	58		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	96	86		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	391	391		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	696	696		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	734	734		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	772	772		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	801	801		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	881	881		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	907	907		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	941	941		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	980	980		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	994	994		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1022	1022		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1045	1045		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1051	1051		N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	1076	1076		N-linked (GlcNAc. .) (Potential).
FT VARSPLIC	453	569		Missing (in isoform 2). /FTid=VSP_010473.
FT CONFLICT	37	37		N -> S (in Ref. 2).
FT CONFLICT	683	683		V -> G (in Ref. 2).
FT SEQUENCE	1153	AA; 127480	MM; 178DB988	ASCB0343 CRC64;

Query Match 77.5%; Score 756; DB 1; Length 1153;
 Best Local Similarity 78.0%; Pred. No. 1.9e-52;
 Matches 149; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY	1	CPQESDIAFLDGGSGIIIPHD	FRMKKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK	60
Db	144	CPQESDIAFLDGGSGIINNIDF	QMKKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFN	203
QY	61	EFQNNPNRSLVKPTITQLLGR	THATGIRKVVRELFINTGARKNAFKILVITDGEKFG	120
Db	204	DFKRNPSRSHVSPIKQLNGR	TKTASGIRKVVRELFKHTNGARENAKILVITDGEKFG	263
QY	121	DLGVEDVIPADREGVIRYIG	VDADPRSKSROELNTIASKPRDHVFNFEALKT	180
Db	264	DELVDKVIDPADRAGVIRYI	GVGNFKNPQSRRELTIASKPAGEHVQVDNFEALNT	323
QY	181	IQNQLREKXFA	191	
Db	324	IQNQLREKXFA	334	

RESULT 4
 Q9J130
 ID Q9J130 PRELIMINARY; PRT; 1151 AA.
 AC Q9J130;
 DT 01-OCT-2000 (TreeBLrel. 15, Created)
 DT 01-OCT-2000 (TreeBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TreeBLrel. 26, Last annotation update)
 DE Integrin beta 2 alpha subunit.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=101116;
RN [1]
RA Fathallah D.M. Sr., Zerria K. Jr.;
RP Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL -!- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC EMBL; AF268593; AAF81280.1; -.
DR HSSP; P11215; 1BHQ.
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR000433; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF00357; Integrin_alpha; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS02242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWA; 1.
KW Cell adhesion; Integrin; Transmembrane.
SQ SEQUENCE 1151 AA; 126943 MW; 8785695D4074CA5 CRC64;

Query Match 74.7%; Score 729; DB 2; Length 1151;
Best Local Similarity 74.3%; Pred. No. 2.9e-50;
Matches 142; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 CPQSDSDIAFLDGSIIIPHPRRKVFSTVMEQLKSKTLFSLMQYSEBFRHFTFK 60
Db 144 CPQSDSDIAFLDGSIIIPHPRRKVFSTVMEQLKSKTLFSLMQYSEBFRHFTFN 203
QY 61 EFQNNPNRSLVKPIQTLQRTHTATGIRKVRLEFNITNGARKNAFKILVITDGERFG 120
Db 204 DFKRNDPKSHVRPIQLNGRTKTASGIRKVRLEFNITNGARKNAFKILVITDGERFG 263
QY 121 DPLGYEDVPEADREGVIRYVGVGDAFSEKSRQSLNTIASKPRPDHVFQNNFEAKT 180
Db 264 DPLNYEDVPEAEAGIIRYVGVGNAGFKPQSRRELDITASKPAGDHVFQVDNFEALNT 323
QY 181 IQNLREKXFA 191
Db 324 IRNLQEKIFA 334

RESULT 5
ITAD RAT STANDARD; PRT; 1161 AA.
AC Q9QVE7;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Integrin alpha-D precursor.
GN Name=Itgad;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RA O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.,
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Gallatin W.M.;
RT "Cloning of rat alpha D, a novel beta 2 integrin.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
CC VCAM1. May play a role in the atherosclerotic process such as
CC clearing lipoproteins from plaques and in phagocytosis of blood-
CC borne pathogens, particulate matter, and senescent erythrocytes
CC from the blood (By similarity).

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CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
CC associates with beta-2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
CC with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF021334; AAF21241.1; -.
DR HSSP; P11215; 1BHQ.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; Integrin_alpha; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR01185; INTEGRINA.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS02242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWA; 1.
KW Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1161 Integrin alpha-D.
FT DOMAIN 20 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Potential.
FT DOMAIN 1122 1161 Cytoplasmic (Potential).
FT REPEAT 34 87 FG-GAP 1.
FT REPEAT 88 87 FG-GAP 2.
FT DOMAIN 152 334 VWFA.
FT REPEAT 352 402 FG-GAP 3.
FT REPEAT 403 454 FG-GAP 4.
FT REPEAT 456 517 FG-GAP 5.
FT REPEAT 519 577 FG-GAP 6.
FT REPEAT 582 634 FG-GAP 7.
FT CA_BIND 467 475 Potential.
FT CA_BIND 531 539 Potential.
FT CA_BIND 594 602 Potential.
FT SITE 1126 1130 GFFKR motif.
FT DISULFID 69 76 By similarity.
FT DISULFID 108 126 By similarity.
FT DISULFID 556 711 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 845 860 By similarity.
FT DISULFID 993 1017 By similarity.
FT DISULFID 1022 1027 By similarity.
FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 696 696 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 734 734 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 784 784 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 907 907 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 936 936 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1045 1045 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1161 AA; 126600 MW; 2258491A984A705E CRC64;

Query Match 62.0%; Score 605; DB 1; Length 1161;
Best Local Similarity 61.3%; Pred. No. 3.2e-40;
Matches 117; Conservative 31; Mismatches 43; Indels 0; Gaps 0;

QY 1 CPQSDSDIAFLDGSIIIPHPRRKVFSTVMEQLKSKTLFSLMQYSEBFRHFTFK 60

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Db 146 CPREMDIAFLIDSGSINQEDFAQMDKDFVXALNGEFASTLFSLMQYKSLIKHTFTT 205
Qy 61 EFQNNPNSRSLVKPITQLGRTHATGIRKVRFLFNITNGARKNAFKILVITDGEKFG 120
Db 206 EFKNILDQSLVDPIVQLGLTYATGIRTVMBELFHSKNGSRKSAKKILLVITDGQYR 265
Qy 121 DPLGYEDVPEADREGVIRVIGVDAPRSEKSKQELNTIASPPRDHVFQVNFALKT 180
Db 266 DPLYSVDIPADKAGIRVIAIGVDAPQETALKELNTIGSAPPQDHVFKVGNFALRS 325
Qy 181 IQNQLREKXFA 191
Db 326 IQRQLQEKIFA 336

RESULT 6
Q63001 PRELIMINARY; PRT; 205 AA.
AC Q63001, 1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
GN Name=itgam;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swistar Kyoto;
RA Nabika T., Ito T., Kitada H., Serikawa T., Mahimo T., Soubrier F.,
RA Julier C., Masuda J., Yamori Y., Nara Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59401; AAB03226.1; -
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Integrin.
FT NON_TER 1 205
FT NON_TER 205 205
SQ SEQUENCE 205 AA; 22922 MW; C8C2D939508DA36 CRC64;

Query Match 60.8%; Score 593; DB 2; Length 205;
Best Local Similarity 74.7%; Pred. No. 4.2e-40;
Matches 121; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

Qy 30 VSTVMEQLKKSKTFLSLMQYSEPRHTPFKEPQNNPNRSLVKPITQLGRTHATGIR 89
Db 1 VSTVMEQPKSKTFLSLMQYSEPRHTPFKEPQNNPNRSLVKPITQLGRTHATGIR 60
Qy 90 KVRLEFNITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRVIGVDAPR 149
Db 61 KVRLEFNITGARKNAFKILVITDGEKFGDPLGYEDVPEADREGVIRVIGVDAPR 120
Qy 150 SEKSRQELNTIASPPRDHVFQVNFALKTIQNQLREKXFA 191
Db 121 KPQSRRELDTIASKPAGDVFQVNFALNTIRNQLQEKIFA 162

RESULT 7
ITAD HUMAN
ID ITAD HUMAN STANDARD; PRT; 1162 AA.
AC Q13349; Q15575; Q15576;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Integrin alpha-D precursor (Leukointegrin alpha D) (CD11d) (ADB2).
GN Name=ITGAD;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96111956; PubMed=8777714;
RA Van der Vliet M., Le Trong H., Wood C.L., Moore P.F., St John T.,
RA Staunton D.E., Gallatin W.M.;
RT "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-3";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [2]
RP IMMUNITY 3:683-690(1995).
RX SEQUENCE OF 1-235 FROM N.A.
RA MEDLINE=20187620; PubMed=10722744;
RA Noti J.D., Johnson A.K., Dillon J.D.;
RT "Structural and functional characterization of the leukocyte integrin gene CBLID. Essential role of Spl and Sp3";
RL J. Biol. Chem. 275:8959-8969(2000).
RN [3]
RP SEQUENCE OF 457-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.A.
RX MEDLINE=96257236; PubMed=8666289;
RA Wong D.A., Davis E.M., LeBeau M., Springer T.A.;
RT "Cloning and chromosomal localization of a novel gene encoding a human beta 2-integrin alpha subunit";
RL Gene 171:291-294(1996).
RN [4]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99059842; PubMed=9841932;
RA Grayson M.H., Van der Vliet M., Sterbinsky S.A., Michael Gallatin W.,
RA Hoffman P.A., Staunton D.E., Bochner B.S.;
RT "alpha beta 2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule 1 (VCAM-1)";
RL J. Exp. Med. 188:2187-2191(1998).
RN [5]
RP INTERACTION WITH VCAM1.
RX MEDLINE=99370002; PubMed=10438935;
RA Van der Vliet M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
RA Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
RT "The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a binding interface between I domain and VCAM-1";
RL J. Immunol. 163:1984-1990(1999).
CC -!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of blood-borne pathogens, particulate matter, and senescent erythrocytes from the blood.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell lines and subsets of peripheral blood leukocytes and strongly on tissue-specialized cells, including macrophages foam cells within atherosclerotic plaques, and on splenic red pulp macrophages.
CC -!- DOMAIN: The integrin I-domain (insert) is a VWA domain. Integrins with I-domains do not undergo protease cleavage.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- SIMILARITY: Contains 1 VWA domain.
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DR EMBL; U37028; AAB38547.1; -
DR EMBL; U40274; AAB60634.1; -
DR EMBL; U40275; AAB60635.1; -
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DR EMBL; U40276; AAB60636.1; --
DR EMBL; U40277; AAB60637.1; --
DR EMBL; U40279; AAB60638.1; --
DR EMBL; U40278; AAB60638.1; JOINED.
DR EMBL; AF187881; AAF62875.1; --
DR HSSP; P11215; 1BHQ.
DR Genew; HGNC:6146; ITGAX.
DR MIM; 602453; --
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR GO; GO:000160; P:cell-matrix adhesion; NAS.
DR GO; GO:006955; P:immune response; NAS.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00092; VWFA; 1.
DR PRINTS; PRO1185; INTEGRINA.
DR PRINTS; PRO0453; VWFADOMAIN.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWFA; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS0234; VWFA; 1.
DR Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
DR Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 1162 Integrin alpha-D.
FT DOMAIN 18 1100 Extracellular (Potential).
FT TRANSMEM 1101 1121 Cytoplasmic (Potential).
FT DOMAIN 1122 1162 FG-GAP 1.
FT REPEAT 32 85 FG-GAP 2.
FT REPEAT 86 ? FG-GAP 2.
FT REPEAT 150 332 VWFA.
FT REPEAT 350 400 FG-GAP 3.
FT REPEAT 401 452 FG-GAP 4.
FT REPEAT 454 516 FG-GAP 5.
FT REPEAT 518 576 FG-GAP 6.
FT REPEAT 581 633 FG-GAP 7.
FT CA_BIND 465 473 Potential.
FT CA_BIND 530 538 Potential.
FT CA_BIND 593 601 Potential.
FT SITE 1127 1131 GPKR motif.
FT DISULFID 67 74 By similarity.
FT DISULFID 105 124 By similarity.
FT DISULFID 655 710 By similarity.
FT DISULFID 769 775 By similarity.
FT DISULFID 846 861 By similarity.
FT DISULFID 994 1018 By similarity.
FT DISULFID 1023 1028 By similarity.
FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 99 99 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 691 691 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 733 733 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 873 873 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 957 957 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1046 1046 N-linked (GlcNAc...) (Potential).
FT CONFLICT 500 500 Missing (in Ref. 2).
FT CONFLICT 515 518 GHFW -> ATP (in Ref. 2).
FT CONFLICT 825 825 L -> V (in Ref. 2).
FT CONFLICT 984 984 V -> A (in Ref. 2).
SQ SEQUENCE 1162 AA; 126885 MW; F296A1A35455D77D CRC64;
Query Match 60.8%; Score 593; DB 1; Length 1162;
Best Local Similarity 60.2%; Pred. No. 3e-39;
Matches 115; Conservative 33; Mismatches 43; Indels 0; Gaps 0;
CY 1 CPQEDSDIAFLDGSGSIIPHDFRRMKEFVSTWMEQLKSKTILFSLMQYSESPRIHFTFK 60
144 CPQENDIVFLDGSGSIQDNDNQMGFGVQAWGQFEGTDILFALMQYSLNLKIHFTFT 203
CY 61 EFQNNPNRSLVPIPTQLGRTHATGIRKRVRELFNITNGARKNAFKILVITDGEKFG 120
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Db 204 QFRTSPSQSLVDPVIVQLKGLTFTATGILTVTLQFHHKNGARKSAKKILIVITDQGYK 263
Qy 121 DPLOYEDVIEADREGVIRVIGVDAPFRSEKROELNTIASPPDRPHVQVNFALKT 180
Db 264 DPLEYSDVIEPQAEKAGIIRYVGVGHAFQGTARQELNTISSAPPQDHFVKNFAALGS 323
Qy 181 IQNQLREKXFA 191
Db 324 IQKOLQEKIVA 334
RESULT 8
ITAX_HUMAN
ID ITAX_HUMAN STANDARD; PRT; 1163 AA.
AC P20702; O81VAG;
DT 01-FEB-1991 (Rel. 17, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
DE alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c) (Leu M5).
GN Name=ITGAX; Synonyms=CD11C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166645; PubMed=3327687;
RA Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A.;
RT "cDNA cloning and complete primary structure of the alpha subunit of a
RT leukocyte adhesion glycoprotein, p150,95."
RL EMBO J. 6:4023-4028(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153906; PubMed=2303426;
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
RT "Genomic structure of an integrin alpha subunit, the leukocyte p150,95
RT molecule."
RL J. Biol. Chem. 265:2782-2788(1990).
RN [3]
RP ERRATUM.
RA Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 20-43.
RX MEDLINE=87167596; PubMed=3549901;
RA Miller L.J., Wiebe M., Springer T.A.;
RT "Purification and alpha subunit N-terminal sequences of human Mac-1
```

RT and p150.95 leukocyte adhesion proteins.";

RL J. Immunol. 138:2381-2383(1987).

CC !- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.

CC !- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.

CC !- SUBCELLULAR LOCATION: Type I membrane protein.

CC !- TISSUE SPECIFICITY: Predominantly expressed in monocytes and granulocytes.

CC !- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

CC !- SIMILARITY: Belongs to the integrin alpha chain family.

CC !- SIMILARITY: Contains 7 FG-GAP repeats.

CC !- SIMILARITY: Contains 1 VWFA domain.

CC !- SIMILARITY: Contains 1 VWFA domain.

CC !- DATABASE: NAME=PROW; NOTE=CD guide CDlic entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdlic.htm".

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M81695; AAA59180.1; --

DR EMBL; M29165; -- NOT ANNOTATED CDS.

DR EMBL; M29487; AAA51620.1; ALT_SEQ.

DR EMBL; M29482; AAA51620.1; JOINED.

DR EMBL; M29483; AAA51620.1; JOINED.

DR EMBL; M29484; AAA51620.1; JOINED.

DR EMBL; M29485; AAA51620.1; JOINED.

DR EMBL; M29486; AAA51620.1; JOINED.

DR EMBL; BC038237; AAH38237.1; --

DR PIR; A36584; RWHLIC.

DR PDB; IN3Y; X-ray; A=141-338.

DR Genew; HGNC:6152; ITGAX.

DR MIM; 151510; --

DR GO; GO:0008305; C:integrin complex; TAS.

DR GO; GO:0004872; P:receptor activity; TAS.

DR GO; GO:0007155; P:cell adhesion; TAS.

DR GO; GO:0009887; P:organogenesis; TAS.

DR InterPro; IPR000413; Integrin_alpha.

DR InterPro; IPR002035; VWFA.

DR Pfam; PF01839; FG-GAP; 3.

DR Pfam; PF00357; Integrin_alpha; 1.

DR Pfam; PF00092; VWFA; 1.

DR PRINTS; PR01185; INTEGRINA.

DR PRINTS; PR00453; VWFA_DOMAIN.

DR SMART; SM00191; Int_alpha; 5.

DR SMART; SM00327; VWFA; 1.

DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

DR PROSITE; PS02334; VWFA; 1.

DR 3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat; Signal; Transmembrane.

KW SIGNAL; 1 19

FT CHAIN 20 1163 Integrin alpha-X.

FT DOMAIN 20 1107 Extracellular (Potential).

FT TRANSMEM 1108 1128 Potential.

FT DOMAIN 1129 1163 Cytoplasmic (Potential).

FT REPEAT 34 87 FG-GAP 1.

FT REPEAT 88 87 FG-GAP 2.

FT DOMAIN 165 351 VWFA.

FT REPEAT ? 401 FG-GAP 3.

FT REPEAT 402 453 FG-GAP 4.

FT REPEAT 455 517 FG-GAP 5.

FT REPEAT 518 576 FG-GAP 6.

FT REPEAT 581 633 FG-GAP 7.

FT REPEAT 666 474 Potential.

FT CA_BIND 530 538 Potential.

FT CA_BIND 593 601 Potential.

FT SITE 1111 1135 GPFKR motif.

FT DISULFID 69 76 By similarity.

FT DISULFID 108 126 By similarity.

FT DISULFID 655 712 By similarity.

FT DISULFID 771 777 By similarity.

FT DISULFID 848 863 By similarity.

FT DISULFID 998 1022 By similarity.

FT DISULFID 1027 1032 By similarity.

FT CARBOHYD 61 61 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 392 392 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 697 697 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 735 735 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 939 939 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1050 1050 N-linked (GlcNAc...) (Potential).

FT VARIANT 48 48 W -> R (in dbSNP:11574633).

FT CONFLICT 209 209 /FTID=VAR_018672.

FT CONFLICT 251 251 T -> S (in Ref. 4).

FT CONFLICT 459 469 T -> A (in Ref. 4).

FT CONFLICT 490 490 T -> S (in Ref. 4).

FT CONFLICT 547 547 G -> A (in Ref. 2).

FT CONFLICT 756 756 E -> K (in Ref. 4).

FT CONFLICT 819 819 D -> L (in Ref. 1).

FT CONFLICT 1161 1163 I -> V (in Ref. 4).

FT STRAND 150 157 SEK -> TPYPQDNV (in Ref. 4).

FT TURN 160 161

FT HELIX 164 178

FT TURN 179 180

FT TURN 183 185

FT STRAND 186 193

FT STRAND 197 201

FT HELIX 203 208

FT HELIX 212 216

FT TURN 217 218

FT STRAND 226 226

FT HELIX 228 236

FT TURN 237 240

FT HELIX 242 244

FT TURN 245 245

FT TURN 248 249

FT STRAND 251 258

FT STRAND 263 263

FT TURN 269 278

FT STRAND 282 288

FT TURN 290 293

FT TURN 296 297

FT HELIX 298 304

FT STRAND 310 312

FT STRAND 313 316

FT HELIX 319 325

FT HELIX 326 334

FT TURN 335 335

SQ SEQUENCE 1163 AA; 127886 MW; 83658A13B5C5DB8F CRC64;

Query Match 56.4%; Score 550; DB 1; Length 1163;

Best Local Similarity 56.0%; Pred. No. 9.1e-36;

Matches 107; Conservative 35; Mismatches 49; Indels 0; Gaps 0;

QY 1 CPQEDSIAFLIDGSGSIIPHDFRMRKFEVSTVMEQLKSKTKLFLSMQYSEEFRIHPTFK 60

DB 145 CPQEQDIVFLIDGSGSISRNFAFMNFAVVISQFQRPSTQSLMQFSNKFQTHTFE 204

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAKILVITDGEKFG 120

DB 205 EFRRTSNFLSLASVHLQGGFTYTATATQNVVHLPHASYGARRDATKILVITDGKEG 264

QY 121 DPLGYEDVTPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRHHVFOVNNFEALKT 180

DB 265 DSLDYKDVIPWADAAGIIRYVIGVLAFQNRNSKWLNDIASKFSQEHFKVDFDALKD 324

Db 266 DNLSYDSVIPMAEAAASIRYAIGVGHKDG 295

RESULT 13
AAH57200

ID AAH57200 PRELIMINARY; PRT; 304 AA.

AC AAH57200;

DT 02-MAR-2004 (TReMBIrel. 27, Created)

DT 02-MAR-2004 (TReMBIrel. 27, Last sequence update)

DT 02-MAR-2004 (TReMBIrel. 27, Last annotation update)

DE Integrin alpha X.

OS Mus musculus (Mouse).

OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/f/;
RC MEDLINE=22389257; PubMed=12477932;
RX Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalls D.B., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RN SEQUENCE FROM N.A.

RP STRAIN=129; TISSUE=Mammary tumor. Brcal-/f/;
RC Strausberg R.;
RL Submitted (Aug-2003) to the ENBL/GenBank/DDBJ databases.
RW ENBL; BC057200; AAH57200.1; -.
KW Integrin.
SQ SEQUENCE 304 AA; 33404 MW; EC52F3EA48FA068D CRC64;

Query Match 41.8%; Score 408; DB 2; Length 304;
Best Local Similarity 53.3%; Pred. No. 6.4e-25;
Matches 80; Conservative 25; Mismatches 43; Indels 2; Gaps 1;

Qy 1 CPORDSDTAFLIDSGSIIIPHDRMKFEVTVMQLKKSKTLFSLMOYSSEFIHFHTFK 60
Db 146 CPKQDIIVLIDSGSSISSTDFEKMLDFVAKNVSQLQPSTRSLMQPSFYRVHTFN 205

Qy 61 EFQNPNPRSLVKPIITQLGRTHATGTRKVVRVLNTINGARKNAFKILVVITGEKFG 120

Db 206 NFISTSPSLSDSVRQLRGVYTASAIAKHVITELFTTQSGAQDATKLVIITDGRKQG 265

Qy 121 DPLGVEDVIPADREGVRYVYG--DAF 148

Db 266 DNLSYDSVIPMAEAAASIRYAIGVGHKDG 295

RESULT 14
Q9WUF8

ID Q9WUF8 PRELIMINARY; PRT; 895 AA.

AC Q9WUF8;

DT 01-NOV-1999 (TReMBIrel. 12, Created)

DT 01-NOV-1999 (TReMBIrel. 12, Last sequence update)

DT 01-JUN-2003 (TReMBIrel. 24, Last annotation update)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2004, 15:29:31 ; Search time 160 Seconds
(without alignments)
428.233 Million cell updates/sec

Title: SEQ1
Perfect score: 976
Sequence: 1 CPQSDDAFLIDSGSIIP.....VNNFEALKTIONQLREKXFA 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	976	100.0	1152	8 ADM99589	Human int
2	976	100.0	1152	8 ADP12435	Protein e
3	976	100.0	1153	2 AAR04136	Alpha sub
4	976	100.0	1153	2 AAW65090	Human Bet
5	976	100.0	1153	3 AAB07360	Human CD1
6	976	100.0	1153	5 AAB080252	Human int
7	976	100.0	1153	5 ABG61469	Human Bet
8	976	100.0	1153	5 AAO14428	Integrin
9	976	100.0	1153	7 ADD25615	Binding d
10	966	99.0	191	5 AAU76856	Human int
11	966	99.0	191	5 AAU76847	Human int
12	960	98.4	187	2 AAY2191	Human com
13	944	96.7	216	4 AAB66786	Amino aci
14	944	96.7	435	2 AAR77461	GST-I-dom
15	893	91.5	177	5 AAU76866	Human int
16	890	91.2	177	5 AAU76865	Human int
17	747	76.5	199	5 ABB78072	Murine I-
18	605	62.0	1151	2 AAW23059	Rat beta
19	605	62.0	1151	2 AAW60001	Rat alpha
20	605	62.0	1151	2 AAW65101	Rat beta-
21	605	62.0	1151	2 AAW72834	Rat alpha
22	605	62.0	1151	2 AAW73344	Rat alpha
23	605	62.0	1151	5 AAB07371	Rat alpha
24	605	62.0	1151	5 ABG61480	Rat Beta2
25	605	62.0	1161	2 AAR78169	Rat alpha

26	605	62.0	1161	2 AAW23062	Rat beta
27	605	62.0	1161	2 AAW60004	Rat alpha
28	605	62.0	1161	2 AAW65104	Rat beta-
29	605	62.0	1161	2 AAW72824	Rat alpha
30	605	62.0	1161	2 AAW73345	Rat alpha
31	605	62.0	1161	3 AAB07374	Rat alpha
32	605	62.0	1161	5 ABG61483	Rat Beta2
33	604	61.9	413	2 AAW23065	Rabbit be
34	604	61.9	413	2 AAW23085	Rabbit be
35	604	61.9	413	2 AAW72839	Rabbit al
36	604	61.9	413	2 AAW73348	Rabbit al
37	604	61.9	413	3 AAB07377	Rabbit al
38	604	61.9	1151	2 AAR78179	Rat alpha
39	602	61.7	413	5 ABG61486	Rabbit Be
40	596	61.1	1155	2 AAR78167	Mouse alp
41	596	61.1	1155	2 AAW23060	Mouse bet
42	596	61.1	1155	2 AAW60002	Mouse alp
43	596	61.1	1155	2 AAW65102	Mouse bet
44	596	61.1	1155	2 AAW72835	Mouse alp
45	596	61.1	1155	2 AAW73346	Mouse alp

ALIGNMENTS

RESULT 1
ADM99589
ID ADM99589 standard; protein; 1152 AA.

XX ADM99589;
XX
XX
XX 17-JUN-2004 (first entry)
XX Human integrin alphaM subunit precursor protein.

XX integrin alpha subunit; beta; antiposrotic; thrombolytic; anticoagulant;
XX osteopathic; cytostatic; immunosuppressive; antiinflammatory;
XX neuroprotective; antisickling; immunotherapy; inflammatory;
XX autoimmune disorder; thrombosis; cancer; osteoporosis;
XX sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
XX alphaM.

XX Homo sapiens.

XX Key Location/Qualifiers
XX FT Misc-difference 965
XX FT Misc /note= "Encoded by CCC"

XX WO2004007530-A2.

XX 22-JAN-2004.

XX 17-JUL-2003; 2003WO-US022301.

XX 17-JUL-2002; 2002US-0396783P.

XX 17-JUL-2002; 2002US-0396790P.

XX 11-SEP-2002; 2002US-0410135P.

XX (BLOO-) CENT BLOOD RES INC.

XX Springer TA, Takagi J;

XX WPI; 2004-122877/12.

XX N-PSDB; ADM99588.

XX Novel modified integrin protein having extracellular domains of integrin

XX alpha and beta subunits or integrin alphaII and beta3 subunit, useful for

XX treating integrin mediated disorders.

XX Disclosure; SEQ ID NO 4; 232pp; English.

XX The invention relates to a novel isolated or recombinant modified

XX integrin protein having extracellular domains of integrin alpha and beta

CC subunits where one of the subunits has one or more mutations, an altered
 CC surface feature or an amino acid substitution or internal deletion,
 CC extracellular domains of the integrin beta subunit that comprise a
 CC mutation that alters a non-cysteine residue to cysteine or extracellular
 CC domains of integrin alpha and beta subunits. The polypeptide of the
 CC invention demonstrates antiproliferative, thrombolytic, anticoagulant,
 CC osteoprotective, cytostatic, immunosuppressive, antiinflammatory,
 CC neuroprotective and anisickling activities and may be useful for
 CC immunotherapy in order to prevent or treat an integrin-mediated disorder
 CC such as an inflammatory disorder, an autoimmune disorder, thrombosis,
 CC cancer, osteoporosis, sickle cell anemia, psoriasis and multiple
 CC sclerosis. The current sequence is that of the human integrin alphaM
 CC subunit precursor protein of the invention.

XX Sequence 1152 AA;

Query Match 100.0%; Score 976; DB 8; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQYSEEPRIHPTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQYSEEPRIHPTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 2

ADP12435
 ID ADP12435 standard; protein; 1152 AA.

AC ADP12435;

DT 12-AUG-2004 (first entry)

DE Protein encoded by mRNA of the invention #45.

KW transplant rejection; immune system; rheumatoid arthritis; lupus;

KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

OS Homo sapiens.

PN WO2004042346-A2.

PD 21-MAY-2004.

PF 24-APR-2003; 2003WO-US012946.

PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

PI Rosenberg S;

DR WPI; 2004-400724/37.

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.

XX

PS Claim 65; SEQ ID NO 2444; 1762pp; English.
 XX The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection, in an
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.

XX Sequence 1152 AA;

Query Match 100.0%; Score 976; DB 8; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQYSEEPRIHPTFK 60
 DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQYSEEPRIHPTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 180

DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSKQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKXFA 191

DB 324 IQNQLREKIFA 334

RESULT 3

AAR04136

ID AAR04136 standard; protein; 1153 AA.

XX AAR04136;

XX 09-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 07-SEP-1990 (first entry)

XX Alpha subunit of Mac-1 leukocyte adhesion receptor.

XX Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;

KW non-specific defence system; integrin gene superfamily.

XX Synthetic.

XX Location/Qualifiers

FT Key 1..16

FT Region /label= signal_peptide

FT Modified-site 86..88

FT /label= putative N-glycosylation site

FT Modified-site 240..242

FT /label= putative N-glycosylation site

FT Modified-site 391..393

FT /label= putative N-glycosylation site

FT Modified-site 469..471

FT /label= putative N-glycosylation site

FT Modified-site 693..695

FT /label= putative N-glycosylation site

FT Modified-site 697..699

FT /label= putative N-glycosylation site

FT Modified-site 735..737

FT /label= putative N-glycosylation site

FT Modified-site 802..804
 FT /label= putative N-glycosylation site
 FT 881..883
 FT /label= putative N-glycosylation site
 FT 901..903
 FT /label= putative N-glycosylation site
 FT 912..914
 FT /label= putative N-glycosylation site
 FT 941..943
 FT /label= putative N-glycosylation site
 FT 947..949
 FT /label= putative N-glycosylation site
 FT 979..981
 FT /label= putative N-glycosylation site
 FT 994..996
 FT /label= putative N-glycosylation site
 FT 1022..1024
 FT /label= putative N-glycosylation site
 FT 1045..1047
 FT /label= putative N-glycosylation site
 FT 1051..1053
 FT /label= putative N-glycosylation site
 FT 1076..1078
 FT /label= putative N-glycosylation site
 FT 1106..1134
 FT /label= putative_transmembrane_region
 FT XX
 PN EP364690-A.
 XX
 XX 25-APR-1990.
 XX
 XX 17-AUG-1989; 89EP-00115159.
 PF
 XX 23-AUG-1988; 88US-00235353.
 PR
 PR 09-MAR-1989; 89US-00321239.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 PA
 XX Springer TA, Corbi A;
 PI
 XX WPI; 1990-125938/17.
 DR
 DR N-PSDB; AAQ04043.
 XX
 XX New pure Mac-1 alpha sub-unit and corresp. DNA - useful for treating
 PT inflammation and viral infections, and in diagnosis.
 PT
 XX Disclosure; Page ?; 3pp; English.

XX Mac-1 alpha subunit is involved in the response to inflammation, i.e.
 CC recognition of and migration to sites of inflammation. It also attaches
 CC to cellular substrates as part of this function making it useful in
 CC visualising endothelial tissue. Mac-1 is a member of the Integrin Gene
 CC superfamily. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
 CC -MAR-2003 to correct PA field.)

CC Revised record issued on 09-SEP-2004 : Correction to feature table key
 CC and pages

XX Sequence 1153 AA;

Query Match 100.0%; Score 976; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 1 CPQSDSDIAFLDGGSGIIPHDFRMKKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 60

DB 144 CPQSDSDIAFLDGGSGIIPHDFRMKKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 203

QY 61 EFQNNPNPSLVKPIQTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNPSLVKPIQTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAFRSEKRSQELNTIASKPPRDHVFQVNNFEALKT 190

DB 264 DPLGYEDVPEADREGVIRYVIGVDAFRSEKRSQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 4

AAW65090
 ID AAW65090 standard; protein; 1153 AA.

XX AAW65090;

XX 28-SEP-1998 (first entry)

XX Human Beta-integrin CD11b subunit protein.

XX Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
 KW type-I diabetes; atherosclerosis; multiple sclerosis; asthma;
 KW lung inflammation; acute respiratory distress syndrome; CD11b subunit;
 KW rheumatoid arthritis.

XX Homo sapiens.

XX US5728533-A.

XX 17-MAR-1998.

XX 07-JUN-1995; 95US-00485618.

PR 23-DEC-1993; 93US-00173497.

PR 05-AUG-1994; 94US-00286889.

PR 21-DEC-1994; 94US-00362852.

XX (ICOS-) ICOS CORP.

XX Van Der Vieren M, Gallatin WM;

XX WPI; 1998-206565/18.

PT Screening assay for modulators of integrin binding - using immobilised or
 PT labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

XX Example 5; Fig 1A-D; 106pp; English.

XX This sequence represents a human beta-integrin CD11b subunit which is
 CC used to describe a method for identifying compounds that modulate the
 CC interaction of the beta-integrin alpha-d subunit with a binding partner
 CC of alpha-d which involves contacting an alpha-d polypeptide with an alpha
 CC -d binding partner, one of which is immobilised and the other of which is
 CC labelled, in the presence of a test compound, and determining if the
 CC compound affects binding between the alpha-d polypeptide and alpha-d
 CC binding partner, where the alpha-d polypeptide is alpha-d or its fragment
 CC comprising the cytoplasmic, transmembrane or extracellular domain of
 CC alpha-d. Compounds that modulate alpha-d binding could be used to treat
 CC diseases such as type-I diabetes, atherosclerosis, multiple sclerosis,
 CC asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
 CC and rheumatoid arthritis

XX Sequence 1153 AA;

Query Match 100.0%; Score 976; DB 2; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQSDSDIAFLDGGSGIIPHDFRMKKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 60

DB 144 CPQSDSDIAFLDGGSGIIPHDFRMKKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTPK 203

QY 61 EFQNNPNPSLVKPIQTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

DB 204 EFQNNPNPSLVKPIQTQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 5
 AAB07360
 ID AAB07360 standard; protein; 1153 AA.
 AC AAB07360;
 DT 17-JAN-2001 (first entry)
 DE Human CD11b protein sequence.
 XX Human; macrophage infiltration inhibition; alpha d integrin;
 KW leukocyte integrin; Leu-CAM; leukointegrin; immune response;
 KW inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes;
 KW atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin;
 KW lung inflammation; acute respiratory distress syndrome; Crohn's disease;
 KW rheumatoid arthritis; central nervous system injury; CD11b.
 XX Homo sapiens.
 OS
 PN WO200029446-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-US0271139.
 PR 16-NOV-1998; 98US-00193043.
 PR 08-JUL-1999; 99US-00350259.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin MW, Van Der Vieren M;
 XX
 DR WPI; 2000-387751/33.
 XX
 PT Use of novel anti-alpha integrin d monoclonal antibodies to inhibit
 PT macrophage infiltration and reduce inflammation at central nervous system
 PT injury sites.
 XX
 PS Example 5; Fig 1; 270pp; English.
 XX
 CC Integrins are a class of membrane-associated molecules that participate
 CC in cellular adhesion. Integrins are made up of an alpha subunit and a
 CC beta subunit. One class of human integrins are restricted to expression
 CC in white blood cells and have a common beta2 subunit: the leukocyte
 CC integrins, Leu-CAMs, leukointegrins or beta2 integrins. Beta2 integrins
 CC have an important role in immune and inflammatory responses. The present
 CC protein sequence is the human integrin alpha subunit CD11b. This sequence
 CC was used in an alignment to identify a novel beta2 integrin alpha
 CC subunit: alpha d (AAA60014 and AAB07359). The present sequence has
 CC approximately 60% identity to the protein sequence of alpha d. The
 CC Alpha d gene and protein may be useful in therapy for diseases linked to
 CC aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple
 CC sclerosis, asthma, psoriasis, lung inflammation, acute respiratory
 CC distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency
 CC (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the
 CC inhibition of macrophage infiltration at the site of a central nervous
 CC system injury. The monoclonal antibodies can also be used to detect and
 CC diagnose Crohn's disease
 XX Sequence 1153 AA;
 SQ

Query Match 100.0%; Score 976; DB 3; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;

Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLDGGSGIIPHDPRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 60
 DB 144 CPQEDSDIAFLDGGSGIIPHDPRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFK 203
 QY 61 EFQNNENPRSLVKPIITQLIGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 204 EFQNNENPRSLVKPIITQLIGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334

RESULT 6
 AAU80252
 ID AAU80252 standard; protein; 1153 AA.
 XX AAU80252;
 AC AAU80252;
 DT 15-JUL-2002 (first entry)
 XX
 DE Human integrin 1 alpha-M subunit protein.
 XX Integrin; antiinflammatory; immunosuppression; nephritis; dermatitis;
 KW inflammatory disease; autoimmune disorder; Crohn's disease;
 KW human immunodeficiency virus; HIV; myocardial infarction;
 KW Sjorgen's syndrome; rheumatoid arthritis.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 499.500
 FT /note= "Encoded by GGG CAG AGG"
 XX
 PN WO200218583-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US027227.
 XX
 PR 01-SEP-2000; 2000US-0229700P.
 XX
 PA (BLOO-) CENT BLOOD RES INC.
 XX
 PI Springer TA, Shimoaka M, Lu C;
 XX
 DR WPI; 2002-382964/41.
 DR N-PSDB; ABK50046.
 XX
 PT Modified integrin-I or integrin I-like domain polypeptide useful as an
 PT immunogen to produce antibodies specific to polypeptide, comprises a
 PT disulfide bond such that polypeptide is stabilized in a desired
 PT conformation.
 XX
 PS Disclosure; Page 109-112; 112pp; English.
 XX
 CC This invention relates to a modified integrin-I or integrin I-like domain
 CC polypeptide comprising at least one disulfide bond so that the domain is
 CC stabilised in a desired conformation. The polypeptide of the invention
 CC may have antiinflammatory or immunosuppressive activities. The
 CC polypeptides of the invention have an open conformation and are useful as
 CC immunogens to produce antibodies that selectively bind to integrin I-
 CC domain; and for identifying a modulator of integrin activity, or of
 CC interaction of an integrin and a cognate ligand. The polypeptide of the
 CC invention, or antibodies (preferably anti-IFA-1 antibody) is useful for
 CC treating or preventing an integrin mediated disorder which is an
 CC inflammatory or autoimmune disorder in a subject and for inhibiting the


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CC binding of an integrin to a cognate ligand such as Crohn's disease.
CC nephritis; human immunodeficiency virus (HIV), myocardial infarction,
CC Sjorgen's syndrome, rheumatoid arthritis, dermatitis. A therapeutic
CC composition comprising the peptide of the invention is useful for
CC treating an integrin mediated disorder in a subject. The polypeptides
CC of integrin-1 alpha-M protein subunit are useful as reagents for diagnosis
CC of integrin-mediated disorders. The present sequence represents the human
CC integrin-1 alpha-M protein subunit used to generate the mutant
CC polypeptides of the invention
XX
SQ Sequence 1153 AA;
  Query Match      100.0%; Score 976; DB 5; Length 1153;
  Best Local Similarity 99.5%; Pred. No. 2.9e-97;
  Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQLKSKTFLSLMQYSEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQLKSKTFLSLMQYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 7
ABG61469
ID ABG61469 standard; protein; 1153 AA.
AC
XX
AC ABG61469;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human Beta2 integrin alphaCD11b subunit.
XX
KW Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD;
KW leukocyte adhesion deficiency; inflammatory response; diabetes;
KW multiple sclerosis; arthritis; graft atherosclerosis; neuroprotective;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory;
KW intracellular cell adhesion molecule; vascular cell adhesion molecule;
KW locomotor recovery; locomotor damage; locomotor impairment;
KW autonomic dysfunction; sensory dysfunction; spinal cord injury.
XX
OS Homo sapiens.
XX
XX WO200230980-A2.
XX
XX PD 18-APR-2002.
XX
XX PF 15-OCT-2001; 2001WO-US032059.
XX
XX PR 13-OCT-2000; 2000US-00688307.
XX
XX FA (ICOS-) ICOS CORP.
XX
XX PI Gallatin WM, Van Der Vieren M;
XX
XX DR WPI; 2002-463260/49.
XX
XX PT Use of an anti-alpha-d monoclonal antibodies for promoting locomotor
XX recovery, inhibiting locomotor damage, limiting locomotor impairment, or
XX PT limiting autonomic and sensory dysfunction following spinal cord injury.
XX
XX PS Example 5; Page 191-194; 270pp; English.

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XX The invention relates to promoting locomotor recovery, inhibiting
XX locomotor damage, limiting locomotor impairment, or limiting autonomic
XX and sensory dysfunction following spinal cord injury by administering an
XX anti-alphaD (Beta2 integrin alpha2 subunit) monoclonal antibody to a
XX spinal cord injury victim. The method also involves the use of a ligand
XX selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule,
XX vascular cell adhesion molecule). The method is useful for promoting
XX locomotor recovery, inhibiting locomotor damage, limiting locomotor
XX impairment, or limiting autonomic and sensory dysfunction following
XX spinal cord injury. In particular, the spinal cord injury comprises
XX compression of the spinal cord. The antibodies are also useful for
XX reducing inflammation at the site of a central nervous system injury. The
XX specification also details the identification of Beta2 integrin alphaD
XX cDNAs and proteins, for use in raising the antibodies. Beta2 integrins
XX are implicated in diseases such as LAD (leukocyte adhesion deficiency,
XX inflammatory response, diabetes, multiple sclerosis, arthritis, graft
XX atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative
XX colitis, immune complex alveolitis and leukaemia. The present sequence is
XX a Beta2 integrin alpha subunit sequence included for comparison with the
XX Beta2 integrin alphaD protein sequences
XX
SQ Sequence 1153 AA;
  Query Match      100.0%; Score 976; DB 5; Length 1153;
  Best Local Similarity 99.5%; Pred. No. 2.9e-97;
  Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQLKSKTFLSLMQYSEFRHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHFRMKFVSTVMEQLKSKTFLSLMQYSEFRHFTFK 203
QY 61 EFQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPIITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 8
AAO14428
ID AAO14428 standard; protein; 1153 AA.
XX
AC AAO14428;
XX
XX 03-MAY-2002 (first entry)
XX
XX DE Integrin Mac-1 alpha subunit.
XX
XX KW Mac-1; integrin alpha subunit; variant integrin inserted domain protein;
XX open conformation; integrin related inflammatory disorder;
XX integrin related immunological disorder; rheumatoid arthritis; ischaemia;
XX reperfusion; hypovolemic shock; infarction; cerebral shock;
XX viral infection; cancer; Gene therapy; vaccine;
XX bioactive agent screening.
XX
XX OS Unidentified.
XX
XX PN WO200204521-A2.
XX
XX PD 17-JAN-2002.
XX
XX PF 09-JUL-2001; 2001WO-US021805.
XX
XX PR 07-JUL-2000; 2000US-0216600P.
XX
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

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PA (BLOO-) CENT BLOOD RES.
 XX Springer T;
 PI WPI; 2002-148167/19.
 DR
 XX
 XX New integrin I domain protein having alteration in at least 2
 PT noncontiguous regions and exits in an open conformation, useful for
 PT treating, preventing or suppressing inflammatory or immunological
 PT disorders.
 XX
 XX Example 1; Fig 1F; 90pp; English.
 PS
 XX The invention comprises structurally biased variant integrin inserted (I)
 CC domain proteins, wherein the alterations to the protein occur in at least
 CC two noncontiguous regions. Specifically the variant integrin I domain
 CC proteins are structurally biased to exist in the open conformation,
 CC thereby altering the binding ability of the protein. The invention also
 CC comprises nucleic acids encoding the variant integrin I domain proteins.
 CC The integrin I domain proteins and nucleic acids are useful for treating,
 CC preventing or suppressing integrin related inflammatory and immunological
 CC disorders (e.g. rheumatoid arthritis). The variant integrin I domain
 CC proteins and nucleic acids can also be used for treating: ischaemia/
 CC reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; vital
 CC infection; and cancer. The variant integrin I domain nucleic acids and
 CC proteins may be used in gene therapy, as vaccines and to screen for
 CC bioactive agents. The present amino acid sequence represents the Mac-1
 CC alpha subunit of integrin
 XX
 SQ Sequence 1153 AA;
 Query Match 100.0%; Score 976; DB 5; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEPRHHTFK 60
 DB 144 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEPRHHTFK 203
 QY 61 EFQNNPNSRLVKPTQLGLGTHATGIRKVRLEFNITNGARNAKILVITDGEKFG 120
 DB 204 EFQNNPNSRLVKPTQLGLGTHATGIRKVRLEFNITNGARNAKILVITDGEKFG 263
 QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPDRHVFQVNNFEALKT 180
 DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSKRSQELNTIASKPPDRHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 DB 324 IQNQLREKIFA 334
 RESULT 9
 ADD25615
 ID ADD25615 standard; protein; 1153 AA.
 AC
 AC ADD25615;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Binding domain-immunoglobulin fusion protein-associated protein #85.
 XX
 KW Binding domain; immunoglobulin; fusion protein; cytostatic;
 KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KW neuroprotective; hinge region; immunoglobulin heavy chain;
 KW CH2 constant region; CH3 constant region; IgG1;
 KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
 KW type 1 diabetes mellitus; multiple sclerosis; autoimmune disease.
 XX
 OS Unidentified.
 XX

PN
 XX
 PD
 XX
 XX 26-JUN-2003.
 PF
 XX 25-JUL-2002; 2002US-00207655.
 XX 17-JAN-2001; 2001US-0367358P.
 PR 17-JAN-2002; 2002US-0003530.
 PR 03-JUN-2002; 2002US-0385691P.
 XX
 PA (GENE-) GENE-CRAFT INC.
 XX
 XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
 XX WPI; 2003-801317/75.
 XX
 PT New binding domain-immunoglobulin fusion protein, useful for treating a
 PT subject having or suspected of having a malignant condition or a B-cell
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
 XX
 PS Disclosure; SEQ ID NO 176; 157pp; English.
 XX
 CC The invention relates to a binding domain-immunoglobulin fusion protein
 CC comprising a binding domain polypeptide that is fused to an
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
 CC CH2 constant region polypeptide that is fused to the hinge region
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
 CC polypeptide that is fused to the CH2 constant region polypeptide. The
 CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
 CC region polypeptide, derived from (a) having 3 or more cysteine residues;
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1
 CC immunoglobulin hinge region polypeptide contains no more than one
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
 CC capable of at least one immunological activity comprising antibody
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
 CC binding domain polypeptide is capable of specifically binding to an
 CC antigen. Also included are an isolated polynucleotide encoding the
 CC binding domain-immunoglobulin fusion protein, a recombinant expression
 CC construct comprising the polynucleotide (operably linked to a promoter),
 CC a host cell transformed or transfected with a recombinant expression
 CC construct, producing the binding domain-immunoglobulin fusion protein, a
 CC pharmaceutical composition comprising the binding domain-immunoglobulin
 CC fusion protein or polynucleotide and a carrier, and treating a subject
 CC having or suspected of having a malignant condition or a B-cell disorder.
 CC The binding domain-immunoglobulin fusion protein is useful for treating a
 CC subject having or suspected of having a malignant condition or a B-cell
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
 CC myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple
 CC sclerosis or autoimmune disease. The present sequence is a binding domain
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The
 CC sequence data for this patent formed part of the printed specification
 CC and is also available in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
 CC identified the sequences in the printed specification by their SEQ ID
 CC number therefore none of the sequences can be explicitly identified.
 XX
 SQ Sequence 1153 AA;
 Query Match 100.0%; Score 976; DB 7; Length 1153;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEPRHHTFK 60
 DB 144 CPQEDSIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEPRHHTFK 203

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRVVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVPEADREGVIRVVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKXFA 334

RESULT 10
AAU76856
ID AAU76856 standard; protein; 191 AA.
XX
AC AAU76856;
DT 21-MAY-2002 (first entry)
XX Human integrin alpha subunit CD11b variant A domain.
DE
XX Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy;
KW mutuin.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 189 /label= Gly, Ala
FT /note= "Wild-type Ile substituted by Gly or Ala"
PT
XX WO200209737-A1.
XX
XX 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
XX WPI; 2002-188687/24.
XX
XX Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
XX Claim 2; Page: 55pp; English.
XX
XX The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the
CC CD11b alpha subunit A domain, where I at residue 320 have been replaced by
CC V at residue 315 and A at residue 320 have been replaced by C, or
CC G or A, F at residue 313 and A at residue 320 have been replaced by C, is useful
CC for determining if a test compound is a candidate compound for binding to
CC CD11b or for treating an inflammatory disorder, by contacting a test
CC compound with the polypeptide and determining if the test compound binds
CC to the polypeptide. The integrin subunits are useful for reducing
CC skeletal muscle injury, for treating disorders caused by ischaemia-
CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
CC to purify variant integrin polypeptide ligands and as bait proteins in
CC two-hybrid or three-hybrid assays. This sequence represents a human

CC integrin alpha subunit CD11b variant A domain. Note: This variant
CC sequence is not featured in the specification but has been derived from
CC the wild-type protein shown in AAU76847
XX
SQ Sequence 191 AA;
Query Match 99.0%; Score 966; DB 5; Length 191;
Best Local Similarity 98.4%; Pred. No. 2.9e-97;
Matches 188; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CPQEDSDIAFLIDSGSIIPHDFFRMKEFVSTVNEQLKSKTILFSLMQYSEFFRIHFTFK 60
DB 1 CPQEDSDIAFLIDSGSIIPHDFFRMKEFVSTVNEQLKSKTILFSLMQYSEFFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
QY 121 DPLGYEDVPEADREGVIRVVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 121 DPLGYEDVPEADREGVIRVVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
QY 181 IQNQLREKXFA 191
DB 181 IQNQLREKXFA 191

RESULT 11
AAU76847
ID AAU76847 standard; protein; 191 AA.
XX
AC AAU76847;
DT 21-MAY-2002 (first entry)
XX
DE Human integrin alpha subunit CD11b A domain.
XX
KW Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..188
FT /note= "This region is specifically claimed"
XX
XX WO200209737-A1.
XX
XX 07-FEB-2002.
XX
XX 31-JUL-2001; 2001WO-US023957.
XX
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Arnaout AM, Li R, Xiong J;
XX WPI; 2002-188687/24.
XX
XX Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases, comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
XX
XX Example 2; Fig 5; 55pp; English.
XX
XX The invention relates to a high affinity integrin polypeptide comprising
CC all or part of a variant integrin alpha subunit A domain or a variant
CC integrin beta subunit A-like domain. The polypeptide, preferably the

CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit CD11b A domain
 XX
 SQ Sequence 191 AA;

Query Match 99.0%; Score 966; DB 5; Length 191;
 Best Local Similarity 97.9%; Pred. No. 2.9e-97;
 Matches 187; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSVTMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 DB 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSVTMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 QY 121 DPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 121 DPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 QY 181 IQNQLREKXFA 191
 DB 181 IQNQLREKIFA 191

RESULT 12
 ID AAY21991 standard; protein; 187 AA.
 AC AAY21991;
 DT 13-SEP-1999 (first entry)
 XX Human complement factor MAC-1 vWF domain sequence.
 DE Factor B analogue; modified; complement activity; complement factor B;
 KW short consensus repeat domain; von Willebrand Factor domain; human; C2;
 KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
 KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
 KW myocardial infarction; acute shock lung syndrome; inflammation; vWF.
 XX Homo sapiens.
 OS US5928892-A.
 PN 27-JUL-1999.
 XX 26-JUL-1996; 96US-00687706.
 XX 03-JAN-1994; 94US-00177109.
 XX (UNIW) UNIV WASHINGTON.
 PA Oglesby TU, Hourcade DE;
 PI WPI; 1999-429498/36.
 DR Nucleic acids encoding complement protein homologues useful for
 PT modulating function of the complement system in the treatment of a
 PT variety of immune and autoimmune complex mediated syndromes.
 XX Disclosure; Fig 5A-B; 53pp; English.

XX The invention relates to a Factor B analogue that exhibits modified
 CC complement activity in vitro. The analogue is generated by substituting a
 CC short consensus repeat domain (SCR) or a von Willebrand Factor domain
 CC (vWF) of human factor B with a SCR or a vWF from a second protein such as
 CC human C2 or CR3. The analogues may be used to regulate the complement
 CC system involved in immune and autoimmune responses. Complement activity
 CC can account for substantial tissue damage in a wide variety of autoimmune
 CC /immune complex mediated syndromes such as lupus erythematosus,
 CC rheumatoid arthritis, hemolytic anemia and myasthenia gravis. Inhibition
 CC of the complement system using the analogues is likely to provide a means
 CC of therapeutic intervention in these cases. Inhibition of complement may
 CC also be favorable in cases that involve tissue damage caused by vascular
 CC injury such as myocardial infarction, cerebral vascular accidents or
 CC acute shock lung syndrome. In these cases the complement system may
 CC contribute to the destruction of partially damaged tissue as in
 CC reperfusion injury. In addition, the use of complement analogues with
 CC novel target specificities could reduce the activity of tissue damaging
 CC proteins at sites of inflammation. Complement inhibition is important in
 CC the prevention of xenograft rejection (the inhibition of complement by
 CC cell-associated and soluble inhibitors is useful in protecting the
 CC transplant from damage caused by activation of endogenous complement. The
 CC present sequence represents the vWF domain of human factor MAC-1
 XX
 SQ Sequence 187 AA;

Query Match 98.4%; Score 960; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.3e-96;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSVTMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 DB 1 CPQEDSDIAFLIDGSGSIIPHDFRMKEFVSVTMEQLKSKTFLSLMOYSEEFRIHFTFK 60
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 DB 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
 QY 121 DPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 DB 121 DPLGYEDVIPADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 QY 181 IQNQLRE 187
 DB 181 IQNQLRE 187

RESULT 13
 AAB66766
 ID AAB66766 standard; protein; 216 AA.
 XX AAB66766;
 XX 10-APR-2001 (first entry)
 DE Amino acids 149-353 of human CR-3 alpha chain and His tag.
 XX EST; expressed sequence tag; inclusion body; binding partner;
 KW immunoglobulins.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200102588-A2.
 XX 11-JAN-2001.
 XX 30-JUN-2000; 2000WO-EP006137.
 XX 02-JUL-1999; 99EP-00112815.
 XX (MORP-) MORPHOSYS AG.

```

PI Frisch C, Kretzschmar T, Hoess A, Von Rueden T;
XX WPI; 2001-147085/15.
XX
XX Generating specific binding partners to (poly)peptides encoded by genomic
XX DNA fragments, involves forming inclusion bodies by expressing the
XX (poly)peptide as part of fusion proteins.
XX
XX Disclosure; Page 18; 45pp; English.
XX
XX The present invention relates to generating a specific binding partner to
XX a peptide, encoded by a genomic DNA fragment or an expressed sequence tag
XX (EST). A nucleic acid molecule encoding a fusion protein is expressed in
XX a host cell to allow the formation of inclusion bodies comprising the
XX fusion protein, the inclusion bodies are isolated and a specific binding
XX partner is generated. The specific binding partners generated are useful
XX for identifying and characterizing naturally occurring proteins e.g. as
XX immunoglobulins or fragments in immunoassays
XX
XX Sequence 216 AA;
XX
XX Query Match 96.7%; Score 944; DB 4; Length 216;
XX Best Local Similarity 99.5%; Pred. No. 8.8e-95;
XX Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 SDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTKFEQNN 65
XX Db 12 SDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTKFEQNN 71
XX
XX QY 66 PNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 125
XX Db 72 PNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 131
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XX QY 126 EDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 185
XX Db 132 EDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 191
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XX QY 186 REKXFA 191
XX Db 192 REKIFA 197
XX
XX RESULT 14
XX AAR77461
XX ID AAR77461 standard; peptide; 435 AA.
XX AC AAR77461;
XX
XX 27-AUG-2003 (revised)
XX 12-FEB-1996 (first entry)
XX
XX GST-I-domain fusion protein.
XX
XX Leukocyte beta-2-integrin Mac-1; I-domain; CD11b; fusion protein;
XX glutathione-S-transferase; GST; Factor-Xa; antiinflammatory.
XX
XX Unidentified.
XX Homo sapiens.
XX Chimeric.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH Protein 1..221
XX FT /label= GST
XX FT 222..228
XX FT /label= Factor-Xa_recognition_sequence
XX FT 225..226
XX FT 229..230
XX FT /label= Spacer
XX FT /note= "spacer allows accommodation of Factor-Xa at the
XX cleavage site"
XX FT 231..235
XX FT Protein
XX FT /label= I-domain

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XX WO9529243-A1.
XX
XX 02-NOV-1995.
XX
XX 19-APR-1995; 95WO-US004439.
XX
XX 26-APR-1994; 94US-00233596.
XX
XX (UPJO ) UPJOHN CO.
XX
XX Heinrichson RL, Anderson DC, Tomich CC, Fairbanks MB;
XX Bajt-Jaeschke ML;
XX
XX WPI; 1995-382991/49.
XX
XX Glutathione-S-transferase fusion protein with Factor Xa cleavage site -
XX for prodn. of I-domain from leukocyte B2-integrin Mac-1.
XX
XX Claim 1; Page 32-34; 41pp; English.
XX
XX A fusion protein comprises a glutathione-S-transferase fusion partner,
XX used to increase the level of soluble protein expression in E. coli and
XX to facilitate affinity purification, and the human leukocyte beta-2-
XX integrin Mac-1 I-domain, linked by a Factor-Xa recognition sequence that
XX allows cleavage of the fusion protein and recovery of the I-domain, which
XX is useful as an antiinflammatory. (Updated on 27-AUG-2003 to correct OS
XX field.)
XX
XX Sequence 435 AA;
XX
XX Query Match 96.7%; Score 944; DB 2; Length 435;
XX Best Local Similarity 99.5%; Pred. No. 2.4e-94;
XX Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 SDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTKFEQNN 65
XX Db 231 SDIAFLIDGSGSIIPHDFRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTKFEQNN 290
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XX QY 66 PNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 125
XX Db 291 PNPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 350
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XX QY 126 EDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 185
XX Db 351 EDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNOL 410
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XX QY 186 REKXFA 191
XX Db 411 REKIFA 416
XX
XX RESULT 15
XX AAU76866
XX ID AAU76866 standard; protein; 177 AA.
XX
XX AAU76866;
XX
XX 21-MAY-2002 (first entry)
XX
XX Human integrin alpha subunit CD11b deletion variant A domain #2.
XX
XX Human; integrin alpha subunit; A domain; CD11b; integrin beta subunit;
XX A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
XX ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
XX antiinflammatory; vasotropic; antiparasitic; vulnary; gene therapy;
XX mutain.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH Key
XX FT Misc-difference 172

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FT /note= "Wild-type Val substituted by Cys"
FT Misc-difference 177
FT /note= "Wild-type Ala substituted by Cys"
XX
PN WO200209737-A1.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US023957.
XX
PR 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00805354.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Arnaout AM, Li R, Xiong J;
XX
DR WPI; 2002-188687/24.
XX
XX
XX The invention relates to a high affinity integrin polypeptide comprising
XX all or part of a variant integrin alpha subunit A domain or a variant
XX integrin beta subunit A-like domain. The polypeptide, preferably the
XX CD11b alpha subunit A domain, where I at residue 332 has been replaced by
XX G or A, F at residue 313 and A at residue 320 have been replaced by C, or
XX V at residue 315 and A at residue 320 have been replaced by C, is useful
XX for determining if a test compound is a candidate compound for binding to
XX CD11b or for treating an inflammatory disorder, by contacting a test
XX compound with the polypeptide and determining if the test compound binds
XX to the polypeptide. The integrin subunits are useful for reducing
XX skeletal muscle injury, for treating disorders caused by ischaemia-
XX reperfusion injury, immune complexes, restenosis and parasitic diseases,
XX to purify variant integrin polypeptide ligands and as bait proteins in
XX two-hybrid or three-hybrid assays. This sequence represents a human
XX integrin alpha subunit CD11b deletion variant A domain. Note: This
XX variant sequence is not featured in the specification but has been
XX derived from the wild-type protein shown in AAU76847
XX
SQ Sequence 177 AA;
Query Match 91.5%; Score 893; DB 5; Length 177;
Best Local Similarity 97.7%; Pred. No. 2.6e-89;
Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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DB 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILWITDGEKFG 120
DB 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILWITDGEKFG 120
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVFQVNNFE 176
DB 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSKQELNTIASKPPRDHVFQVNNFE 176
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Search completed: November 9, 2004, 15:32:20
Job time : 161 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: November 9, 2004, 15:36:01 ; Search time 153 Seconds

(without alignments)
440.955 Million cell updates/sec

Title: SEQ1

Perfect score: 976

Sequence: 1 CPQEDSDIAFLDGSIIIP.....VNFPEALTIQNLREKXFA 191

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	976	100.0	191	10	US-09-805-354-1
2	976	100.0	191	11	US-09-758-493-1
3	976	100.0	191	14	US-10-144-259-1
4	976	100.0	1153	9	US-09-945-265-4
5	976	100.0	1153	9	US-09-350-259-3
6	976	100.0	1153	10	US-09-902-481A-1
7	976	100.0	1153	10	US-09-891-943-3
8	976	100.0	1153	14	US-10-144-259-30
9	976	100.0	1153	14	US-10-207-655-176
10	967	99.1	1137	10	US-09-902-481A-6
11	961	98.5	1137	10	US-09-902-481A-5
12	951	97.4	1137	10	US-09-902-481A-4
13	950	97.3	187	15	US-10-345-863-37

14 950 97.3 187 16 US-10-615-515-9 Sequence 9, Appli
15 944 96.7 190 15 US-10-346-863-42 Sequence 42, Appli
16 944 96.7 190 15 US-10-346-863-48 Sequence 48, Appli
17 944 96.7 216 10 US-09-795-872-5 Sequence 5, Appli
18 944 96.7 216 15 US-10-662-824-5 Sequence 5, Appli
19 939 96.2 184 15 US-10-346-863-17 Sequence 17, Appli
20 938 96.1 1137 10 US-09-902-481A-3 Sequence 3, Appli
21 747 76.5 199 14 US-10-066-551-11 Sequence 11, Appli
22 605 62.0 1151 9 US-09-350-259-37 Sequence 37, Appli
23 605 62.0 1151 9 US-09-891-943-37 Sequence 37, Appli
24 605 62.0 1161 9 US-09-350-259-55 Sequence 55, Appli
25 605 62.0 1161 10 US-09-891-943-55 Sequence 55, Appli
26 604 61.9 413 9 US-09-350-259-101 Sequence 101, App
27 604 61.9 413 10 US-09-891-943-101 Sequence 101, App
28 596 61.1 1155 9 US-09-350-259-46 Sequence 46, Appli
29 596 61.1 1155 10 US-09-891-943-46 Sequence 46, Appli
30 596 61.1 1161 9 US-09-350-259-53 Sequence 53, Appli
31 596 61.1 1161 10 US-09-891-943-53 Sequence 53, Appli
32 593 60.8 191 10 US-09-805-354-3 Sequence 3, Appli
33 593 60.8 191 11 US-09-758-493-3 Sequence 3, Appli
34 593 60.8 191 14 US-10-144-259-3 Sequence 3, Appli
35 593 60.8 1161 9 US-09-350-259-2 Sequence 2, Appli
36 593 60.8 1161 9 US-09-350-259-99 Sequence 99, Appli
37 593 60.8 1161 10 US-09-891-943-2 Sequence 2, Appli
38 593 60.8 1161 10 US-09-891-943-99 Sequence 99, Appli
39 552 56.6 1163 9 US-09-350-259-4 Sequence 4, Appli
40 552 56.6 1163 10 US-09-891-943-4 Sequence 4, Appli
41 550 56.4 191 10 US-09-805-354-2 Sequence 2, Appli
42 550 56.4 191 11 US-09-758-493-2 Sequence 2, Appli
43 550 56.4 191 14 US-10-144-259-2 Sequence 2, Appli
44 550 56.4 1163 14 US-10-116-275-204 Sequence 204, App
45 374 38.3 264 9 US-09-350-259-93 Sequence 93, Appli

ALIGNMENTS

RESULT 1

US-09-805-354-1
; Sequence 1, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnacut, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/221,950
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-1

Query Match 100.0%; Score 976; DB 10; Length 191;
Best Local Similarity 99.5%; Pred. No. 3.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLDGSIIIPHDFFRMKEFVSTVMEQLKSKTLPFLMOYSEEPRIHFTFK 60
DB 1 CPQEDSDIAFLDGSIIIPHDFFRMKEFVSTVMEQLKSKTLPFLMOYSEEPRIHFTFK 60
QY 61 BFQNNPRLSVKPIITOLLGRTHATGIRKVRFLFNITNGARKNAFKILVITDGBKFG 120
DB 61 BFQNNPRLSVKPIITOLLGRTHATGIRKVRFLFNITNGARKNAFKILVITDGBKFG 120


```

; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20020062008A1e1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-350-259-3

Query Match      100.0%; Score 976; DB 9; Length 1153;
Best Local Similarity 99.5%; Pred. No. 3.7e-93;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 7
US-09-891-943-3
; Sequence 3, Application US/09891943
; Publication No. US20030077278A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. US20030077278A1e1 Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/891,943
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-891-943-3

Query Match      100.0%; Score 976; DB 10; Length 1153;
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Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 8
US-10-144-259-30
; Sequence 30, Application US/10144259
; Publication No. US20030109691A1

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-5

Query Match      98.5%; Score 961; DB 10; Length 1137;
Best Local Similarity 95.3%; Pred. No. 1.4e-91;
Matches 182; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTWEOQLKSKTILFSLMQYSEEFRIHFTFK 60
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QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247

QY 121 DPLGYEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307

QY 181 IQNOLREKXFA 191
DB 308 IQNOLREKIFA 318

RESULT 12
US-09-902-481A-4
; Sequence 4, Application US/09902481A
; Publication No. US20030054440A1
; GENERAL INFORMATION:
; APPLICANT: Springer, Timothy
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Shifman, Julia
; TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
; FILE REFERENCE: A-70586-1/RT/RMS/RMK
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/216,600
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-902-481A-4

Query Match      97.4%; Score 951; DB 10; Length 1137;
Best Local Similarity 94.8%; Pred. No. 1.6e-90;
Matches 181; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTWEOQLKSKTILFSLMQYSEEFRIHFTFK 60
DB 128 CPQEDSDIAFLIDGSGSIIPHDPRRMKEFVSTWEOQLKSKTILFSLMQYSEEFRIHFTFK 187

QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 188 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 247

QY 121 DPLGYEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 248 DPLGYEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 307

QY 181 IQNOLREKXFA 191
DB 308 IQNOLREKIFA 318
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```
RESULT 13
US-10-346-863-37
; Sequence 37, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US/10/346,863
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-37

Query Match      97.3%; Score 950; DB 15; Length 187;
Best Local Similarity 99.5%; Pred. No. 1.6e-91;
Matches 186; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DSDIAFLIDGSGSIIPHDPRRMKEFVSTWEOQLKSKTILFSLMQYSEEFRIHFTFK 64
DB 1 DSDIAFLIDGSGSIIPHDPRRMKEFVSTWEOQLKSKTILFSLMQYSEEFRIHFTFK 60

QY 65 NPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 124
DB 61 NPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120

QY 125 YEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 184
DB 121 YEDVIPADREGVIRVIGVGDADFSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180

QY 185 LREKXFA 191
DB 181 LREKIFA 187

RESULT 14
US-10-615-515-9
; Sequence 9, Application US/10615515
; Publication No. US20040132974A1
; GENERAL INFORMATION:
; APPLICANT: FAGAN, RICHARD, JOSEPH
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2004
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: PCT/GB02/00107
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: GB 0100750.9
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-615-515-9

Query Match      97.3%; Score 950; DB 16; Length 187;
Best Local Similarity 99.5%; Pred. No. 1.6e-91;
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Matches 186; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 64
   |||||
Db 1 DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 60
   |||||
QY 65 NNPRSLVKPITQLLGRHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 124
   |||||
Db 61 NNPRSLVKPITQLLGRHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLG 120
   |||||
QY 125 YEDVIPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKTIQNQ 184
   |||||
Db 121 YEDVIPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKTIQNQ 180
   |||||
QY 185 LREKFA 191
   |||||
Db 181 LREKFA 187

```

RESULT 15

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US-10-346-863-42
; Sequence 42, Application US/10346863
; Publication NO. US2004003825A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Variable amino acid
US-10-346-863-42

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Query Match          96.7%; Score 944; DB 15; Length 190;
Best Local Similarity 99.5%; Pred. No. 7.1e-91;
Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 65
   |||||
Db 2 SDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTFKFQN 61
   |||||
QY 66 NNPRSLVKPITQLLGRHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 125
   |||||
Db 62 NNPRSLVKPITQLLGRHTATGIRKVVRELFNITNGARKNAFKILVITDGEKFGDPLGY 121
   |||||
QY 126 EDVIPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKTIONOL 185
   |||||
Db 122 EDVIPEADREGVIRYVIGVDAFRSEKSRQELNTIASKPPRDHVQVNNFEALKTIONOL 181
   |||||
QY 186 REKFA 191
   |||||
Db 182 REKFA 187

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Search completed: November 9, 2004, 15:48:59
Job time : 154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2004, 15:29:33 ; Search time 38 Seconds
(without alignments)
333.335 Million cell updates/sec

Title: SEQ1
Perfect score: 976
Sequence: 1 CQEDSDIAFLIDSGSIIP.....VNNFEALKTIONQLREKXFA 191

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 56318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	976	100.0	1152	2	US-08-476-062A-43
2	976	100.0	1152	5	PCT-US96-01314-43
3	976	100.0	1152	6	5424399-2
4	976	100.0	1153	1	US-08-173-497-3
5	976	100.0	1153	1	US-08-286-889-3
6	976	100.0	1153	1	US-08-485-618-3
7	976	100.0	1153	1	US-08-382-852-3
8	976	100.0	1153	2	US-08-605-672-3
9	976	100.0	1153	2	US-08-482-293A-3
10	976	100.0	1153	2	US-08-943-363-3
11	976	100.0	1153	3	US-09-193-043-3
12	976	100.0	1153	4	US-09-688-307A-3
13	976	100.0	1153	4	US-09-350-259-3
14	960	98.4	187	2	US-08-177-109A-61
15	960	98.4	187	2	US-08-687-706-61
16	944	96.7	216	4	US-09-795-872-5
17	944	96.7	435	5	PCT-US95-04439-1
18	605	62.0	1151	1	US-08-286-889-37
19	605	62.0	1151	1	US-08-485-618-37
20	605	62.0	1151	1	US-08-382-852-37
21	605	62.0	1151	2	US-08-605-672-37
22	605	62.0	1151	2	US-08-482-293A-37
23	605	62.0	1151	2	US-08-943-363-37
24	605	62.0	1151	3	US-09-193-043-37
25	605	62.0	1151	4	US-09-688-307A-37
26	605	62.0	1151	4	US-09-350-259-37
27	605	62.0	1161	1	US-08-485-618-55

28	605	62.0	1161	1	US-08-362-652-55
29	605	62.0	1161	2	US-08-605-672-55
30	605	62.0	1161	2	US-08-482-293A-55
31	605	62.0	1161	2	US-08-943-363-55
32	605	62.0	1161	3	US-09-193-043-55
33	605	62.0	1161	4	US-09-688-307A-55
34	605	62.0	1161	4	US-09-350-259-55
35	604	61.9	413	1	US-08-485-618-101
36	604	61.9	413	2	US-08-605-672-101
37	604	61.9	413	2	US-08-482-293A-101
38	604	61.9	413	3	US-08-943-363-101
39	604	61.9	413	3	US-09-193-043-101
40	604	61.9	413	4	US-09-688-307A-101
41	604	61.9	413	4	US-09-350-259-101
42	596	61.1	1155	1	US-08-286-889-46
43	596	61.1	1155	1	US-08-485-618-46
44	596	61.1	1155	1	US-08-362-652-46
45	596	61.1	1155	2	US-08-605-672-46

ALIGNMENTS

RESULT 1
US-08-476-062A-43
; Sequence 43, Application US/08476062A
; Patent No. 5877275
; GENERAL INFORMATION:
; APPLICANT: Arianout, M. Amin
; TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
; TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,062A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,081
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: 07/637,830
; FILING DATE: 04-JAN-1991
; APPLICATION NUMBER: 07/539,842
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: 07/212,573
; FILING DATE: 28-JUN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/068003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-476-062A-43

Query Match 100.0%; Score 976; DB 2; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 8.1e-94;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 Db 264 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 Db 324 IQNQLREKIFA 334

RESULT 2

PCT-US96-01314-43
 ; Sequence 43, Application PC/TUS9601314
 ; GENERAL INFORMATION:
 ; APPLICANT: M. Amin Arnaut
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 ; NUMBER OF SEQUENCES: 78
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/01314
 ; FILING DATE: 30-JAN-96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/380,167
 ; FILING DATE: 30-JAN-95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: John W. Freeman
 ; REGISTRATION NUMBER: 29,066
 ; REFERENCE/DOCKET NUMBER: 00786/267001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1152
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 PCT-US96-01314-43

Query Match 100.0%; Score 976; DB 5; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 8.1e-94;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120

Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 Db 264 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 Db 324 IQNQLREKIFA 334
 RESULT 3
 5424399-2
 ; Patent No. 5424399
 ; APPLICANT: ARNAOUT, M. AMIN
 ; TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
 ; NUMBER OF SEQUENCES: 12
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/78,871
 ; FILING DATE: 16-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 539,842
 ; FILING DATE: 18-JUN-1990
 ; APPLICATION NUMBER: 212,573
 ; FILING DATE: 28-JUN-1988
 ; SEQ ID NO: 2:
 ; LENGTH: 1152
 5424399-2

Query Match 100.0%; Score 976; DB 6; Length 1152;
 Best Local Similarity 99.5%; Pred. No. 8.1e-94;
 Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 60
 Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSSEFRIHFTFK 203
 QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
 Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
 QY 121 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
 Db 264 DPLGYEDVPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
 QY 181 IQNQLREKXFA 191
 Db 324 IQNQLREKIFA 334

RESULT 4

US-08-173-497-3
 ; Sequence 3, Application US/08173497
 ; Patent No. 5437958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Van Der Vieren, Monica
 ; TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
 ; TITLE OF INVENTION: Subunit
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 S. Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No 5437958and, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-173-497-3

Query Match 100.0%; Score 976; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 5
US-08-286-889-3
Sequence 3, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-3

Query Match 100.0%; Score 976; DB 1; Length 1153;
Best Local Similarity 99.5%; Pred. No. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTLFSLMOYSEEFRIHFTFK 203

QY 61 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263

QY 121 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323

QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 6
US-08-485-618-3
Sequence 3, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; US-08-485-618-3
;
; Query Match 100.0%; Score 976; DB 1; Length 1153;
; Best Local Similarity 99.5%; Pred. No. 8.1e-94;
; Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
; Db 144 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203
;
; QY 61 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
; Db 204 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
;
; QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
; Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
;
; QY 181 IQNQLREKXFA 191
; Db 324 IQNQLREKIFA 334
;
; RESULT 7
; US-08-362-652-3
; Sequence 3, Application US/08362652
; Patent No. 5766850
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun,
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,652
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; US-08-362-652-3
;
; Query Match 100.0%; Score 976; DB 1; Length 1153;
; Best Local Similarity 99.5%; Pred. No. 8.1e-94;
; Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 60
; Db 144 CPQEDSDIAFLIDGSGSIIPHDFRRMKFVSTVMEQLKSKTFLSLMQYSEEFRIHFTFK 203
;
; QY 61 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
; Db 204 EFQNNPNRSLVKPIITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
;
; QY 121 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
; Db 264 DPLGYEDVPEADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
;
; QY 181 IQNQLREKXFA 191
; Db 324 IQNQLREKIFA 334
;
; RESULT 8
; US-08-605-672-3
; Sequence 3, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun,
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 1153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-605-672-3

Query Match      100.0%; Score 976; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRRMKEFVSTWMEQLKSKTILFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDSGSIIIPHDFRRMKEFVSTWMEQLKSKTILFSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRVIGVDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRVIGVDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 9
US-08-482-293A-3
; Sequence 3, Application US/08482293A
; Patent No. 5831029
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482.293A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-293A-3

Query Match      100.0%; Score 976; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. No. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDSGSIIIPHDFRRMKEFVSTWMEQLKSKTILFSLMQYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDSGSIIIPHDFRRMKEFVSTWMEQLKSKTILFSLMQYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRVIGVDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALKT 180
Db 264 DPLGYEDVIPADREGVIRVIGVDAPFRSEKSRQELNTIASPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 10
US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,363
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1153 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-3

Query Match      100.0%; Score 976; DB 2; Length 1153;
Best Local Similarity 99.5%; Pred. NO. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

RESULT 11
US-09-193-043-3
; Sequence 3, Application US/09193043
; Patent No. 6251395
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; TITLE OF INVENTION: No. 6251395el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/193,043
; PRIOR FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3

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Query Match      100.0%; Score 976; DB 3; Length 1153;
Best Local Similarity 99.5%; Pred. NO. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

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RESULT 12
US-09-688-307A-3
; Sequence 3, Application US/09688307A
; Patent No. 6432404
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6432404el Human Beta-2
; FILE REFERENCE: 27866/36646
; CURRENT APPLICATION NUMBER: US/09/688,307A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/193,043
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 08/605,672
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/173,497
; PRIOR FILING DATE: 1993-12-23
; PRIOR APPLICATION NUMBER: 08/286,889
; PRIOR FILING DATE: 1994-08-05
; PRIOR APPLICATION NUMBER: 08/362,652
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/943,363
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-307A-3

Query Match      100.0%; Score 976; DB 4; Length 1153;
Best Local Similarity 99.5%; Pred. NO. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 60
Db 144 CPQEDSDIAFLIDGSGSIIPHDPRMKEFVSTVMEQLKSKTFLSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 120
Db 204 EFQNNPNRSLVKPITQLLGRTHATGIRKVVRELFNTNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 180
Db 264 DPLGYEDVPEADREGVIRYVIGVDAPRSEKSRQELNTIASKPRDRHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
Db 324 IQNQLREKIFA 334

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RESULT 13
US-09-350-259-3
; Sequence 3, Application US/09350259
; Patent No. 6620915
; GENERAL INFORMATION:
; APPLICANT: Gallatin, Michael W.
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 6620915el Human 2
; FILE REFERENCE: 27866/35004
; CURRENT APPLICATION NUMBER: US/09/350,259
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: 09/193,043
; EARLIER FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: 08/173,497
; EARLIER FILING DATE: 1993-12-23
; EARLIER APPLICATION NUMBER: 08/286,889
; EARLIER FILING DATE: 1994-08-05
; EARLIER APPLICATION NUMBER: 08/362,652
; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363

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; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-259-3

Query Match      100.0%; Score 976; DB 4; Length 1153;
Best Local Similarity 99.5%; Pred. No. 8.1e-94;
Matches 190; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 60
DB 144 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 203
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 14
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-61

Query Match      98.4%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334

RESULT 15
US-08-687-706-61
; Sequence 61, Application US/08687706
; Patent No. 5928892
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-687-706-61

Query Match      98.4%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.6e-93;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 60
DB 1 CPQEDSDIAFLIDGSGSIIPHDFFRMKEFVSTVMEQLKSKTFLFSLMOYSEEFRIHFTFK 60
QY 61 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 120
DB 204 EFQNNPNRSLVKPITQLLGRTHGTATGIRKVVRELFNITNGARKNAFKILVITDGEKFG 263
QY 121 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 180
DB 264 DPLGYEDVIPADREGVIRYVIGVDAPFRSEKSRQELNTIASKPPRDHVFQVNNFEALKT 323
QY 181 IQNQLREKXFA 191
DB 324 IQNQLREKIFA 334
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Db	61	EFQNNPNSLVKPIQLLGRTHATGIRKVVRELFNITNGARKNAFKILVWITDGEKFG	120
QY	121	DPLGYEDVIPEADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
Db	121	DPLGYEDVIPEADREGVIRYVIGVGDAFSEKSRQELNTIASKPPRDHVFQVNNFEALKT	180
QY	181	IQNQLRE	187
Db	181	IQNQLRE	187

Search completed: November 9, 2004, 15:36:38
Job time : 39 secs